

ATTACHMENTS

RESULT 1
 AAA89399 Standard; cDNA; 270 BP.
 XX
 ID AAA89399
 AC AAA89399;
 XX
 DT 11-SEP-2003 (revised)
 DT 23-APR-2001 (first entry)
 XX
 DE Scorpion sodium channel agonist cDNA clone ibj1c.pk008.f14.
 XX
 KW Scorpion; venom; toxin; sodium channel agonist; anticonvulsant;
 KW potassium channel antagonist; convulsant; insecticide; conotoxin;

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed.

四百零二

Result %	Query				DB				Description	
	No.	Score	Match Length	ID	DB	Length	DB	ID		
	1	42.2	23.6	270	5	AAB89399	Scorpion	Aaa89399	Scorpion	
	2	40.8	22.8	270	5	AAB89400	Scorpion	Aaa89400	Scorpion	
	3	40.8	22.8	270	5	AAB89398	Scorpion	Aaa89398	Scorpion	
	4	38	21.2	270	5	AAB89397	Scorpion	Aaa89397	Scorpion	
c	5	32.6	18.2	336	2	AAT90799	Rat pers	Aat90799	Rat pers	
c	6	32.6	18.2	336	2	AAX60455	Partial	Aax60455	Partial	
c	7	32.6	18.2	336	2	AAX60459	Partial	Aax60459	Partial	
c	8	32.6	18.2	391	2	AAX60460	W0991423	Aax60460	W0991423	
c	9	32.6	18.2	515	8	ABP53533	Aspergil	Abz53533	Aspergil	
c	10	32	17.9	780	4	ABA89006	Bacillus	Aba89006	Bacillus	
c	11	32	17.9	2489	6	ABT78877	E. coli	Abt78877	E. coli	
c	12	32	17.9	2489	10	ABH80444	Escheri	Adh80444	Escheri	
c	13	32	17.9	2498	4	ABA89004	Drosophi	Aba89004	Drosophi	
c	14	32	17.9	2811	4	ABU25174	Drosophi	Abu25174	Drosophi	
c	15	31	17.3	4590	5	AAH24065	Yeast AO	Aah24065	Yeast AO	
c	16	30.6	17.1	582	6	ABN63438	Human ca	Abn63438	Human ca	
c	17	30.4	17.0	13563	4	ABU06306	Drosophi	Abu06306	Drosophi	
c	18	30.4	17.0	13629	4	ABD06290	Drosophi	Abd06290	Drosophi	
c	19	30.2	16.9	473	3	ACG98441	Human co	Acg98441	Human co	
c	20	30.2	16.9	1037	4	ABD34174	Human	Abd34174	Human	

xx
BS Claim 1(a); Page 57: 6000; English

XX PI Herrmann R, Lee J, Wong JF;
 XX DR WPI; 2001-050111/06.
 DR P-PSDB; AAB20076.

XX New isolated polynucleotide encoding a scorpion toxin for treating epilepsy, degenerative disorders such as Huntington's disease, and neuronal death following stroke, and for creating plants that are insect-tolerant.

XX PS Claim 1(a); Page 57; 60pp; English.

CC The present sequence is that of a portion of the cDNA insert in clone ibj1c.pk006.p4 that encodes a protein showing 29.6% identity to an insecticidal toxin of *Orthochirus scrobiculus*. The clone was isolated from a scorpion (*Buthotus judaicus*) telson cDNA library. The invention provides isolated nucleic acid sequences (see AAB89386-400) encoding scorpion toxins (see AAB20064-78) that are sodium channel modifiers. The invention also relates to the construction of a chimeric gene encoding all or part of the sodium channel modifier, in sense or antisense orientation, where expression of the chimeric gene results in production of altered levels of the sodium channel modifier in a transformed host cell. Sodium channel modifiers can be used to treat neurological problems involving abnormal functioning of excitatory amino acid synapses, e.g., epilepsy, Huntington's disease and neuronal death following stroke. Genetically engineered recombinant baculoviruses which express protein toxins capable of incapacitating an insect host can be used as biological insecticides. The nucleic acids can be used to create transgenic plants in which sodium channel agonists of the invention are expressed for improved insect tolerance. (Updated on 11-SEP-2003 to standardise OS field)

XX SQ Sequence 270 BP; 82 A; 34 C; 58 G; 96 T; 0 U; 0 Other;

Query Match 22.8%; Score 40.8; DB 5; Length 270;
 Best Local Similarity 61.1%; Pred. No. 0.00038;
 Matches 66; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Db 130 CCTTCCAACTCTGGTGAATTCTGAAAGATGGTGAAGCTTGTGG 190
 Qy 130 CCTTCCAACTCTGGTGAATTCTGAAAGATGGTGAAGCTTGTGG 177
 Db 191 TCACCTCGTGTGTTGTTGTTGATTGAAAGAACATAATT 238

Db 100 ATTAATCGGACTGATCATTAGATCTGTCAGAACACGGTAGCTAACG 129
 Qy 131 ATCATGATATTGCGGACATTTGAAGTACATGGTGAATTGGTGG 190
 Db 132 TTCCCBATGCTGCTGTAATTCTGAAAGGTGAACTGAGGTCT 177
 Qy 132 TTCCCBATGCTGCTGTAATTCTGAAAGGTGAACTGAGGTCT 177
 Db 193 ACCCTGTTGTTGTTGAAATTGAAAGAACATCGATAATT 238

RESULT 4
 AAA89397 ID AAA89397 standard; cDNA; 270 BP.
 AC AAA89397;
 XX DT 11-SEP-2003 (revised)
 DT 23-APR-2001 (first entry)
 XX OS Scorpion sodium channel agonist cDNA clone ibj1c.pk0004.h3.

KW Scorpion; venom; toxin; sodium channel agonist; anticonvulsant;
 KW nootropic; cerebroprotective; insecticide; ss.

XX Hottentotta judaica.

XX Key Location/Qualifiers
 FH sig_peptide 1..63
 PT / *tag= a
 PT mat_peptide 64..267
 PT / *tag= a

XX PN WO200078957-A2.
 XX PD 28-DEC-2000.

XX XX XX PR 21-JUN-2000; 20000W0-US017048.
 XX XX PA (DUP0) DU PONT DE NEMOURS & CO E I.
 XX PI Hermann R, Lee J, Wong JF;
 XX DR WPI; 2001-050111/06.
 DR P-PSDB; AAB20075.

XX New isolated polynucleotide encoding a scorpion toxin for treating epilepsy, degenerative disorders such as Huntington's disease, and neuronal death following stroke, and for creating plants that are insect-tolerant.

XX PS Claim 1(a); Page 56; 60pp; English.

CC The present sequence is that of a portion of the cDNA insert in clone ibj1c.pk004.h3 that encodes a protein showing 29.7% identity to an insecticidal toxin of *Orthochirus scrobiculus*. The clone was isolated from a scorpion (*Buthotus judaicus*) telson cDNA library. The invention provides isolated nucleic acid sequences (see AAB89386-400) encoding scorpion toxins (see AAB20064-78) that are sodium channel modifiers. The invention also relates to the construction of a chimeric gene encoding all or part of the sodium channel modifier, in sense or antisense orientation, where expression of the chimeric gene results in production of altered levels of the sodium channel modifier in a transformed host cell. Sodium channel modifiers can be used to treat neurological problems involving abnormal functioning of excitatory amino acid synapses, e.g., epilepsy, Huntington's disease and neuronal death following stroke. Genetically engineered recombinant baculoviruses which express protein toxins capable of incapacitating an insect host can be used as biological insecticides. The nucleic acids can be used to create transgenic plants in which sodium channel agonists of the invention are expressed for improved insect tolerance. (Updated on 11-SEP-2003 to standardise OS field)

XX SQ Sequence 270 BP; 84 A; 33 C; 57 G; 96 T; 0 U; 0 Other;

Query Match 21.2%; Score 38; DB 5;
 Best Local Similarity 56.0%; Pred. No. 0.0039;
 Matches 93; Conservative 0; Mismatches 70; Indels 3; Gaps 1;

Db 72 AATCCGGACTGCAATTAGATCTGTCAGAACACGGTAGCTAACG 131
 Qy 12 CCGGAAACTACCACTGATTCCTGGCAAACTACCTGGGTTGGAGAT 71
 Db 76 CCAGGAAATTACCGATATCTGTTATGTTAGCTTAAATCAT 135

Db 136 AAT---TATGTTGTTGACATTGATCTGTTATGTTAGCTAACAGCTTAAATCAT 136

Db 132 TTCCCBATGCTGCTGTAATTCTGAAAGGTGAACTGAGGTCT 177

Qy 132 TTCCCBATGCTGCTGTAATTCTGAAAGGTGAACTGAGGTCT 177

Db 193 ACCCTGTTGTTGTTGAAATTGAAAGAACATCGATAATT 238

RESULT 5
 AAT80799/c
 ID AAT80799 standard; cDNA; 336 BP.
 XX AC AAT80799;
 XX AC AAT80799;
 XX DT 27-MAR-1998 (first entry)
 XX DE Rat persephin cDNA fragment.
 XX KW Persephin; neurturin; glial-derived neurotrophic factor; GDNF;
 KW neuronal degeneration; haemopoietic cell degeneration;
 KW cardiac muscle degeneration; therapy; rat; ss.
 XX OS Rattus sp.

OS Rattus sp.
 XX WO9914235-A1.
 PN 25-MAR-1999.
 PD 15-SEP-1998; 98W0-US019163.
 XX 16-SEP-1997; 97US-00931858.
 PR Unidentified.
 XX WO914235-A1.
 PA (UNIW) UNIV WASHINGTON.
 XX PI Johnson EM, Milbrandt JD, Kotzbauer PT, Lampe PA, Klein R;
 PI Desauvage F;
 XX DR 1999-244023/20.
 XX PT New isolated persephin growth factor nucleic acids used to, e.g. promote neuronal growth.
 XX PS Example; Page 159; 222pp; English.
 XX The invention relates to a novel isolated and purified growth factor (GF) that comprises persephin or a fragment or a conservatively substituted variant. The persephin GF polypeptides can promote the survival and growth of neurons and non-neuronal cells. The persephin GF polypeptides or polynucleotides can be used for preventing or treating cellular degeneration or insufficiency, e.g. neuronal degeneration resulting from peripheral neuropathy, amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease, ischemic stroke, acute brain injury, acute spinal cord injury, nervous system tumour, multiple sclerosis, or infection, hematopoietic cell degeneration or insufficiency resulting from eosinopenia, anaemia, thrombocytopenia, or stem-cell insufficiencies, cardiac muscle degeneration or insufficiency resulting from cardiomyopathy or congestive heart failure. They can also be used for treating e.g. peripheral nerve trauma or injury, exposure to neurotoxins, metabolic diseases such as diabetes or renal dysfunctions and damage caused by infectious agents. The GF can also be used for promoting the growth and/or differentiation of a cell in a culture medium. The antisense polynucleotides can be used for treating a disease condition mediated by expression of persephin by a population of cells. The products can also be used for detection and diagnosis.

XX Sequence 336 BP; 77 A; 91 C; 98 G; 70 T; 0 U; 0 Other;
 XX Score 32.6; DB 2; Length 336;
 Best Local Similarity 52.6%; Pred. No. 0.37; Matches 71; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

XX SQ 25 CACTGATTCCTCCGACAATACCTACCTGCGGCCCTTGGGAGATAATCCGGACTTGCA 84
 Db 285 CACCTGAGCCTTCAAAGGTGCTTGTGATTGTGAGAACGGCTGGC 226
 Qy 85 TTAAAGATCTGTCAAAACACGGTGGATAACGGTTACGGTTATTGCTAGCCCTCCAATGCTGGT 144
 Db 225 TTCCAGCCACACGCCAACGGCTGGCTGAGGTGAGCTGCAATGGTGGT 166
 Qy 145 GTGAATTCTGAAGG 159
 Db 165 GGTCTCAAGGAAGG 151

RESULT 8
 AAX0460/C DT 17-AUG-1999 (first entry)
 ID XX DE WO9914235 Seq ID No: 107.
 XX KW Growth factor; GF; persephin; neuron growth; cellular degeneration;

Query Match 18.2%; Score 32.6; DB 2; Length 391;
 Best Local Similarity 52.6%; Pred. No. 0.39; Matches 0; Mismatches 64; Indels 0; Gaps 0;
 Matches 71; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 25 CACTGATTCCTCCGACAATACCTACCTGCGGCCCTTGGGAGATAATCCGGACTTGCA 84
 Db 337 CACCTGAGCCTTCAAAGGTGCTTGTGATTGTGAGAACGGCTGGC 278
 Qy 85 TTAAAGATCTGTCAAAACACGGTGGATAACGGTTACGGTTATTGCTAGCCCTCCAATGCTGGT 144
 Db 277 TTCCAGCCACACGCCAACGGCTGGCTGAGGTGAGCTGCAATGGTGGT 218
 Qy 145 GTGAATTCTGAAGG 159
 Db 217 GGTCTCAAGGAAGG 203

RESULT 9
 AB253533 ID AB253533 Standard; CDNA; 515 BP.
 XX AC KW AB253533;

XX 28-MAR-2003 (first entry)
 XX Aspergillus oryzae polynucleotide SEQ ID NO 2646.
 XX Aspergillus oryzae; fermentation; fungus; industrial; EST;
 KW expressed sequence tag; gene; ss.
 OS Aspergillus oryzae.
 XX WO200270476-A1.
 XX PD 10-OCT-2002.
 XX PF 22-MAR-2002; 2002WO-IB000890.
 XX PR 30-MAR-2001; 2001EP-00098371.
 XX PA (NRAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (NARE-) NAT RES INST BREWING.
 PA (NRQ) NAT FOOD RES INST MIN AGRIC.
 XX PI Machida M, Akita O, Kashiwagi Y, Kitamoto K, Horiuchi H;
 PI Takeuchi M, Kobayashi T, Kitamoto N, Gomi K, Abe K;
 DR WPI; 2003-046817/04.
 XX PT Detection of expression of specific Aspergillus genes for monitoring the
 PT fermentation and growth conditions of the fungus, using DNA probes.
 XX PS SEQ ID NO 2646; 48pp + Sequence Listing; Japanese.
 CC The invention relates to a polynucleotide having any of 6006 specific
 CC sequences (ABZ50888-ABZ56893), which are expressed by a fungus under
 CC specific culture conditions including one or more of eutrophic,
 CC oligotrophic, solid, early germination, alkaline, high temperature, low
 CC temperature or maltose culture or polynucleotides stringently hybridising
 CC to these sequences. The polynucleotides are useful for monitoring the
 CC progress of fermentation and the growth conditions of a fungus,
 CC especially of Aspergillus oryzae which is widely used in industrial
 CC fermentation. Also monitoring for fungal contamination. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp://wipo.int/pub/published_pct_sequences
 XX SQ Sequence 515 BP; 124 A; 138 C; 135 G; 118 T; 0 U; 0 Other;
 Query Match Score 18.2%; Best Local Similarity 52.6%; Pred. No. 0_43; Matches 71; Conservative 0; Nismatches 64; Indels 0; Gaps 0;
 QY 37 CCGACAATTACCTACTGTGGCCCTTTCGGAGATAATCGGACTGATTAAGATCTGC 96
 DB 192 CGGTCCACAGCCTGGTGAAGCCATTATCGGTGCAATGGGTGACATGATGTC 251
 QY 97 AGAACACCGTGTGATTAACGGPATGGTACGGCTTCAGTGGTGAATTCTGA 156
 DB 252 GTCTCGTCCGTGAGGAATTGGGAAGTGGCTATGCCGAGGGGTGAATTCGAGA 311
 QY 157 AGGATGAGAACGTGA 171
 DB 312 AGTGTGGGCTTGA 326
 RESULT 10
 AB89005/c
 ID AB89006 standard; DNA; 780 BP.
 XX AC AB89006;
 DT 11-FEB-2002 (first entry)
 XX DT Escherichia coli polynucleotide SEQ ID NO 581.
 DE Escherichia coli.
 XX XX Escherichia coli; B2/D+A-; antiinflammatory; antibacterial;
 KW immunosuppressive; extra-intestinal infection; phylogeny; meningitis;
 KW systemic infection; non-diarrhoeal infection; septicaemia;
 KW pyelonephritis; antibiotic resistance; ds.
 OS Escherichia coli.
 XX XX WO200166572-A2.
 PN XX PR 13-SEP-2001.
 XX PF 12-MAR-2001; 2001WO-EP003445.
 XX PR 10-MAR-2000; 2000FR-00003145.
 PR 02-FEB-2001; 2001FR-00001449.
 XX PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PI Bingen E, Bonacorsi S, Clermont O, Nassif X, Tinsley C;
 XX DR WPI; 2001-550253/61.
 PT A library of DNA fragments of Escherichia coli strains for the phylogenetic
 PT determination of a given strain comprises polynucleotides of nature B2/D+
 A-.
 XX PS Example 6; Fig 6; 646BP; English.
 CC The invention relates to a library of DNA fragments of Escherichia coli
 CC strains comprising polynucleotides (ABA88577-ABA88729 and ABA889533) and
 CC encoded proteins (ABB2459-ABB5291 and ABB5294-ABB53094) of nature
 CC B2/D+A-. The polynucleotides have potential antiinflammatory,
 CC antibacterial and immunosuppressive activity as part of pharmaceutical
 CC compositions used to treat, palliate or prevent extra-intestinal E. coli
 CC infections. The polypeptides are useful for determining the phylogenetic
 CC group of a given E. coli strain. These polypeptides can detect and treat
 CC an undesired development of E. coli, particularly an extra-intestinal
 CC infection that include systemic and non-diarrhoeal infections such as
 CC septicæmia, pyelonephritis and meningitis this is particularly
 CC advantageous as bacterial resistance is increasing with the more frequent
 CC use of broad spectrum antibiotics
 XX SQ Sequence 780 BP; 223 A; 171 C; 195 G; 191 T; 0 U; 0 Other;
 Query Match Score 32; DB 4; Length 780;
 Best Local Similarity 58.3%; Pred. No. 0_84;
 Matches 56; Conservative 0; Nismatches 40; Indels 0; Gaps 0;
 QY 33 TCTTCGGCAATACCTACTGTGGCTTCTTGAGATAATCGGACTGCTTAAGATC 92
 DB 246 TCCTGGCCAATATGTCCTGACCATCGAGCCGAGCTAAATATGTCATATC 187
 QY 93 TGTCAGAAACACGGTGTGATTAACGGPATTTGTCAC 128
 DB 186 TTTCGGTAATCGTAAGTGTTCAGGTATTGAAAC 151
 RESULT 11
 AB878877 standard; DNA; 2489 BP.
 ID AB878877;
 XX AC AB878877;
 XX DT 17-DEC-2002 (first entry)
 XX DE E. coli CFT073 genomic sequence #44.
 XX KW Pathogenic; Escherichia coli CFT073 infection; livestock; pyelonephritis;
 KW urinary tract infection; open reading frame; ORF; uropathogenic;
 KW antibacterial; arthropathic; nephrotropic; gene; ds.
 XX OS Escherichia coli.

XX WO200259320-A2.
 XX PI Blattner FR, Welch RA, Burland VD;
 XX DR XX
 PD 01-AUG-2002.
 XX WPI: 2001-863398/80.

XX PT New nucleic acid of Escherichia coli CFT073, useful for preparing a composition for diagnosing, treating or preventing infection caused by Escherichia coli CFT073.

XX PT
 PA (WISC-) WISCONSIN ALUMNI RES FOUND.
 XX PS Claim 1; SEQ ID NO 44; 4pp; English.
 XX
 CC The invention relates to an isolated Escherichia coli CFT073 nucleic acid molecule. The nucleic acid is useful for preparing a composition for diagnosing, treating or preventing infection caused by Escherichia coli CFT073. The present sequence represents a contig of the Escherichia coli CFT073 genome that is not present in Escherichia coli K-12.
 CC
 XX SQ Sequence 2489 BP; 668 A; 563 C; 578 G; 677 T; 0 U; 3 Other;

PS Query Match 17.9%; Score 32; DB 10; Length 2489;
 Best Local Similarity 58.3%; Pred. No. 1.3;
 Matches 56; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

CC Qy 33 TCTTCCGACATACTACCTACTCTGGGAGATAATCCCGACTCATTAAGATC 92
 Db 901 TCTGGGCCATACTCCCTGACCATCAGGCCATCATTCAGGCCAGTGCAATATC 960

CC Qy 93 TGTCAAGAAACACGGTTACGGTATTGCTAC 128
 Db 961 TTTCGGTAATCGTAAGTGTTCAGGTATTGAAC 996

XX RESULT 13
 SQ Sequence 2489 BP; 668 A; 563 C; 578 G; 677 T; 0 U; 3 Other;
 PS Query Match 17.9%; Score 32; DB 6; Length 2489;
 Best Local Similarity 58.3%; Pred. No. 1.3;
 Matches 56; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

CC Qy 33 TCTTCCGACATACTACCTACTCTGGGAGATAATCCCGACTCATTAAGATC 92
 Db 901 TCTGGGCCATACTCCCTGACCATCAGGCCATCATTCAGGCCATCATTC 960

CC Qy 93 TGTCAAGAAACACGGTTACGGTATTGCTAC 128
 Db 961 TTTCGGTAATCGTAAGTGTTCAGGTATTGAAC 996

XX RESULT 14
 ADH0444 ID ADH0444 standard; DNA; 2489 BP.
 XX AC ADH0444;
 XX DT 22-APR-2004 (first entry)
 DE Escherichia coli CFT073 genome contig #44.
 KW ds; gene; Escherichia coli; CFT073; Escherichia coli CFT073 infection.
 KW Escherichia coli; CFT073.
 PN US2003165870-A1.
 XX 04-SEP-2003.
 XX PF 01-MAR-2002; 2002US-00085959.
 XX PR 01-MAR-2002; 2002US-00085959.
 XX PA (BLAT/) BLATTNER F R.
 PA (WELCH) WELCH R A.
 PA (BURLD/) BURLAND V D.

XX PT A library of DNA fragments of Escherichia coli strains for the phylogenetic determination of a given strain comprises polynucleotides of nature B2/D+
 PT A-.

XX PS Example 6; Fig 6; 646pp; English.

XX CC The invention relates to a library of DNA fragments of Escherichia coli strains comprising polynucleotides (ABA8857-ABA88729 and ABA8533) and CC encoded proteins (ABB52159-ABB52919 and ABB53094) of nature CC

CC B2/D+A- The polynucleotides have potential antiinflammatory,
 CC antibacterial and immunosuppressive activity as part of pharmaceutical
 CC compositions used to treat, palliate or prevent extra-intestinal E. coli
 CC infections. The polypeptides are useful for determining the phylogenetic
 CC group of a given E. coli strain. These polypeptides can detect and treat
 CC an undesired development of E. coli, particularly an extra-intestinal
 CC infection that include systemic and non-diarrhoeal infections such as
 CC septicemia, pyelonephritis and meningitis. This is particularly
 CC advantageous as bacterial resistance is increasing with the more frequent
 CC use of broad spectrum antibiotics

Sequence 2498 BP; 673 A; 563 C; 580 G; 682 T; 0 U; 0 Other;

Query Match 17.9%; Score 32; DB 4; Length 2498;
 Best Local Similarity 58.3%; Pred. No. 1.3;

Matches 56; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 33 TCTTCGAGATAACCTACTGTGCCCTTGAGATAATCGGACTGCATAAGTC 92
 DB 906 TCTGGCGCAATAGTCCGTGACCATCAGGCCAGTGTAAATGATGCCATAC 965

QY 93 TGTCAGAACACGGTGTGGAATTACGGTTTGTCTAC 128
 DB 966 TTTCGGTAATCGTAAGTGTTCAGGTTAGTGTGARAC 1001

RESULT 14
 AB25174/C
 ID AB25174 standard; DNA; 2811 BP.
 XX

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 26995.

XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ds.

XX Drosophila melanogaster.

OS WO0017042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX WPI; 2001-656860/75.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 genes from Drosophila and for elucidating cell signaling and cell-cell
 interactions.

PT PI Venter JC, Adams M, Li PWD, Myers EW;

XX XX

Claim 1: SEQ ID NO 26995; 21PP + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176 -ABL3051), expressed DNA
 CC sequences (ABL0180-ABL16175) and the encoded proteins (ABL577/3-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

SQ	Sequence 2811 BP; 719 A; 640 C; 660 G; 792 T; 0 U; 0 Other;	SQ	Sequence 2811 BP; 719 A; 640 C; 660 G; 792 T; 0 U; 0 Other;
	Query Match 17.9%; Score 32; DB 4; Length 2811;		Query Match 17.9%; Score 32; DB 4; Length 2811;
	Best Local Similarity 58.3%; Pred. No. 1.4;		Best Local Similarity 58.3%;保守 Matches 56; Conservation 0; Mismatches 40; Indels 0; Gaps 0;
QY	1 CGCTTGAGTCGGGAAACTACCCACTGATTCTCGACAAATACCTACCTGCGGCC 60	QY	1 CGCTTGAGTCGGGAAACTACCCACTGATTCTCGACAAATACCTACCTGCGGCC 60
Db	2672 CTCCTGAGCCCAAGATAATTACCAAGATACTGGCATACAATCTCAGTCCTGC 2613	Db	2672 CTCCTGAGCCCAAGATAATTACCAAGATACTGGCATACAATCTCAGTCCTGC 2613
QY	61 CTTTGGGGATAATCCGACTGCATTAAGATCTGTC 96	QY	61 CTTTGGGGATAATCCGACTGCATTAAGATCTGTC 96
Db	2612 CCTTGAGCTTATCCTCGCTCGTTAAGTTGGCC 2577	Db	2612 CCTTGAGCTTATCCTCGCTCGTTAAGTTGGCC 2577
	RESULT 15		
	AAH24065/C		
	ID AAH24065 standard; DNA; 4590 BP.		
	XX		
	AAH24065;		
	XX		
	29-AUG-2001 (first entry)		
	DT		
	XX		
	DE Yeast AOD9604-associated DNA sequence, SEQ ID NO:1.		
	XX		
	KW Human growth hormone analogue peptide; hGH; AOD9604; lipid metabolism;		
	KW modulation; lipolysis stimulation; hormone-sensitive lipase stimulation;		
	KW lipogenesis inhibition; acetyl CoA carboxylase inhibition; obesity;		
	KW functional food; transgenic yeast; fat/lean ratio; food use; ds.		
	XX		
	OS Saccharomyces cerevisiae.		
	XX		
	Key Location/Qualifier		
	PH		
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	FT /*tag= a		
	FT /note= "Represented as * in the specification"		
	FT misc_feature 3617		
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	FT misc_feature 3941		

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OM protein - protein search, using bw model

Run on: July 8, 2005, 15:22:21 ; Search time 177 Seconds
 (without alignments)
 167.800 Million cell updates/sec

Title: US-10-617-978-20

Perfect score: 343

Sequence: 1 ADVPGNYPLDSSDNTYLCAP.....GYCYAFQCWCEFLKDENVKV 58

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03_*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description	
1	PS8752	64.7	58	1	BIRT_PARTH	Parabuthus mesobuthus	
2	Q6WJF5	54.8	80	2	SCX_CENNO	Q6WJF5 centruroides	
3	Q6VAY9	37.0	67	1	SCM_CENSC	Q6VAY9 centruroides	
4	Q6VAY9	35.9	64	2	SCX2_CENSC	Q6VAY9 centruroides	
5	Q6VAY8	11.5	34.8	65	1	SCM_CENSC	Q6VAY8 centruroides
6	Q6VAY8	11.7	34.1	64	1	SCX2_CENSC	Q6VAY8 centruroides
7	Q6VAY8	11.7	34.1	87	1	SCX3_CENSC	Q6VAY8 centruroides
8	Q6VAY0	11.6	33.8	64	2	SCX3_CENSC	Q6VAY0 centruroides
9	Q6VAY4	11.6	33.8	64	2	SCX2_CENSC	Q6VAY4 centruroides
10	Q6VAY4	11.5	33.5	64	2	SCX2_CENSC	Q6VAY4 centruroides
11	Q6VAY7	11.5	33.5	73	2	SCX2_CENSC	Q6VAY7 centruroides
12	Q6VAY7	11.5	33.5	85	1	SCX7_CENLL	Q6VAY7 centruroides
13	Q6VAY7	11.5	33.5	85	1	SCX7_CENLL	Q6VAY7 centruroides
14	Q6VAY4	11.3	32.9	66	2	SCX2_CENSC	Q6VAY4 centruroides
15	Q6VAY0	11.3	32.9	67	2	SCX2_CENSC	Q6VAY0 centruroides
16	Q6VAY4	11.3	32.9	87	1	SCX2_CENLL	Q6VAY4 centruroides
17	Q6VAY4	11.1	32.4	87	1	SCX2_CENNO	Q6VAY4 centruroides
18	Q6VAY4	11.0	32.1	66	1	SCX2_CENNO	Q6VAY4 centruroides
19	Q6VAY4	11.0	32.1	87	1	SCX3_CENSC	Q6VAY4 centruroides
20	Q6VAY3	10.9	31.8	64	2	SCX2_CENSC	Q6VAY3 centruroides
21	Q6VAY3	10.9	31.8	66	1	SCX2_CENLL	Q6VAY3 centruroides
22	Q6VAY4	10.9	31.8	87	1	SCX2_CENNO	Q6VAY4 centruroides
23	Q6VAY4	10.8	31.5	62	1	SCX2_CENNO	Q6VAY4 centruroides
24	Q6VAY4	10.8	31.5	66	1	SCX2_CENLL	Q6VAY4 centruroides
25	Q6VAY4	10.8	31.5	84	1	SCX2_CENNO	Q6VAY4 centruroides
26	Q6VAY1	10.7	31.2	64	2	SCX2_CENNO	Q6VAY1 centruroides
27	Q6VAY2	10.7	31.2	64	2	SCX2_CENNO	Q6VAY2 centruroides
28	Q6VAY6	10.7	31.2	64	2	SCX2_CENNO	Q6VAY6 centruroides
29	Q6VAY6	10.7	31.2	66	1	SCX1_CENLI	Q6VAY6 centruroides
30	Q6VAY6	10.7	31.2	66	1	SCX1_CENLI	Q6VAY6 centruroides
31	Q6VAY4	10.7	31.2	66	1	SCX1_CENLI	Q6VAY4 centruroides

ALIGNMENTS

RESULT 1									
BIRT_PARTH		STANDARD		PRT;		58 AA.			
ID	P58752;								
AC									
DT	28-FEB-2003	(Rel. 41, Created)							
DT	28-FEB-2003	(Rel. 41, Last sequence update)							
DT	05-JUL-2004	(Rel. 44, Last annotation update)							
DE	Birtoxin.								
OS	Parabuthus transvaalicus (South African Fat-tail scorpion).								
OC	Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;								
OC	Buthiida; Buthoidea; Buthiidae; Parabuthus.								
NCBI_TaxID	170972;								
RN	[1]								
RP	SEQUENCE.								
RC	TISSUE_Venom;								
RX	Medline=21518524; PubMed=11606203;								
RA	Inceoglu B., Lango J., Wu J., Hawkins P., Southern J., Hammock B.D.;								
RT	"Isolation and characterization of a novel type of neurotoxic peptide from the venom of the South African scorpion Parabuthus transvaalicus (Buthidae).";								
RT	Eur. J. Biochem. 268:5407-5413(2001).								
CC	-I- FUNCTION: Binds to sodium channels, thereby blocking neuronal transmission								
CC	(By similarity). Moderately toxic, but very high abundant. Lethal to mice. Do not target repilin channels.								
CC	-I- SUBCELLULAR LOCATION: Secreted.								
CC	-I- TISSUE SPECIFICITY: Expressed by the venom gland.								
CC	-I- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.								
DR	HS35P; P41964; IMYN.								
DR	InterPro: IPR002061; Scorpion_toxin1.								
DR	Pram; PF00537; Toxin_3.								
DR	ProDom; PD00908; Scorpion_toxinL.								
KW	Direct protein sequencing; Ionic channel inhibitor; Toxin.								
KW	Sodium channel inhibitor; Toxin.								
FT	DISULFID	18	41						
FT	DISULFID	27	46						
FT	DISULFID	31	48						
SQ	SEQUENCE	58 AA:	654 MW;						
Qy	1 ADVPGNYPLDSSDNTYLAPLGNDPDCIKICORHGVDYGYCYAQFCWCEFLDENKV 58								
Qy	1 ADVPGNYPLDSSDNTYLAPLGNDPDCIKICORHGVDYGYCYAQFCWCEFLDENKV 58								
Db	1 ADVPGNYPLDSSDNTYLAPLGNDPDCIKICORHGVDYGYCYAQFCWCEFLDENKV 58								

RESULT 2

Q6WJF5

ID Q6WJF5 PRELIMINARY; PRT; 80 AA.

AC Q6WJF5; AC Q6WJF5; DT 05-JUL-2004 (TREMBLref. 27, Created)

DT 05-JUL-2004 (TREMBLref. 27, Last sequence update)

DR 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DB Toxin precursor

OS Mesobuthus martensii (Manchurian scorpion) (Butihus martensi).

CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;

CC Butihida; Buthoidea; Butihidae; Mesobuthus.

NCI_TaxID=34649;

RN [1]

RP SEQUENCE FROM N.A.

RC Jiang D., Cao Z., Li W.; Submitted (APR-2003) to the EMBL/GenBank/DDJB databases.

CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

DR EMBL; AAQ22733.1; -.

DR GO; GO:0005576; C: extracellular; IEA.

DR GO; GO:0008200; P: ion channel inhibitor activity; IEA.

DR GO; GO:0009405; P: pathogenesis; IEA.

DR InterPro; IPR002051; Scorpion_toxinL.

DR Pfam; PF00537; Toxin_3_1.

DR ProDom; PD000908; Scorpion_toxinL; 1.

KW SIGNAL.

FT CHAIN 1 22 Potential.

FT SIGNAL 1 22 Potential.

FT CHAIN 23 80 MW; 5298A57F1A62905 CRC64;

SEQUENCE 80 AA; 9274 MW;

Query Match Score 186; DB 2; Length 80;

Best Local Similarity 54.4%; Pred. No. 3e-14;

Matches 31; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Qy 2 DVPEVYPLDSSDTNTLCPLGNDPDCIKICQKHDVYCYAFQCWCFLKDENVK 58

Do 24 DDPPQPTMAGNRYKTCITLGENEYCRICKLKGVTIGCYNNSRCWCFLKDVTI 80

RESULT 3

SCXC_CENNO STANDARD; PRT; 67 AA.

SCXC_CENNO ID P63079;

AC DT 25-OCT-2004 (Rel. 45, Created)

AC DT 25-OCT-2004 (Rel. 45, Last sequence update)

AC DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Neurotoxin Cn12.

OS Centruroides noxius (Mexican scorpion).

CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;

CC Butihida; Buthoidea; Butihidae; Centruroides.

NCI_TaxID=66778;

RN [1]

RP SEQUENCE, MASS SPECTROMTRY, AND STRUCTURE BY NMR.

TISSUE="PMID:15182366; DOI=10.1111/j.1432-1033.2004.04181.x; Coronas F.V., del Rio-Portilla F., Hernandez-Marin E., Pimienta G., Corrales L.D.; Zamudio F.Z., Rodriguez de la Vega R.C., Wanke E., Possani L.D.";

CC "NMR solution structure of Cn12, a novel peptide from the Mexican scorpion Centruroides noxius with a typical beta-toxin sequence but with alpha-like physiological activity.";

Eur. J. Biochem. 271:2504-2516 (2004).

CC -!- FUNCTION: Binds, in vitro, to sodium channels and inhibits the inactivation of the activated channels. Seems not toxic to mice, crickets and sweet-water shrimps.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family. Beta-toxin subfamily.

CC PDB; 1BPA; NMR; A-1-67.

CC 3D-structure; Direct protein sequencing; Ionic channel inhibitor;

KW DISULFID 11 65

FT DISULFID 15 40

FT DISULFID 25 45

FT DISULFID 29 47

SEQUENCE 67 AA; 7148 MW; B7BCAE8566FEC0BC CRC64;

Query Match Score 127; DB 1; Length 67;

Best Local Similarity 46.2%; Pred. No. 3.e-07;

Matches 24; Conservative 10; Mismatches 16; Indels 2; Gaps 2;

Qy 7 YPLDSSDTNTLCPLGNDPDCIKICQKHDVYCYAFQCWCFLKDENVK 56

Db 4 YPLASNGCKFGSGLGENNPNICNAVEKKASGYDGYCAYTVCYCHVAEGTV 55

RESULT 4

Q6V4Y9 PRELIMINARY; PRT; 64 AA.

Q6V4Y9 ID Q6V4Y9; PRELIMINARY; PRT; 64 AA.

AC Q6V4Y9; PRELIMINARY; PRT; 64 AA.

DR 05-JUL-2004 (TrEMBLrel. 27, Created)

DR 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DR 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Beta-toxin (Fragment).

OS Centruroides sculpturatus (Bark scorpion).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;

OC Butihida; Buthoidea; Butihidae; Centruroides.

NCBI_TaxID=218467;

RN [1]

RP SEQUENCE FROM N.A.

RA Zhu S.; Submitted (JUL-2003) to the EMBL/GenBank/DDJB databases.

RL CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

DR EMBL; AY351301; AAR08036.1; -.

DR HSSP; P01493; 1UZA.

DR GO; GO:0005576; C: extracellular; IEA.

DR GO; GO:0008200; P: ion channel inhibitor activity; IEA.

DR GO; GO:0005515; P: protein binding; IEA.

DR GO; GO:005952; P: defense response; IEA.

DR GO; GO:0009405; P: pathogenesis; IEA.

DR InterPro; IPR003614; Knot1.

DR InterPro; IPR001219; Neurotoxin.

DR Pfam; PF00377; Toxin_3_1.

DR PRINTS; PRO0285; SCORPNTOXIN.

DR PRINTS; PRO0284; TOXIN.

DR ProDom; PD000906; Scorpion_toxinL_1.

DR SMART; SM00505; Knot1; 1.

FT NON-TER 1

FT NON-TER 64 64

SEQUENCE 64 AA; 6959 MW; 73009293C661C41 CRC64;

Query Match Score 123; DB 2; Length 64;

Best Local Similarity 46.9%; Pred. No. 8.e-07;

Matches 23; Conservative 6; Mismatches 18; Indels 2; Gaps 1;

Qy 7 YPLDSSDTNTLCPLGNDPDCIKICQKHDVYCYAFQCWCFLKD 53

Db 4 YLVNSTGCKYGLKGENEGCDKECKAKNQGSYGYCAYFACWCGLPE 52

RESULT 5

SCXC_CENSC STANDARD; PRT; 65 AA.

SCXC_CENSC ID SCXC_CENSC

AC DT 15-JUL-1999 (Rel. 38, Created)

AC DT 15-JUL-1999 (Rel. 38, Last sequence update)

DE Toxin CSB_M1 (CBM1) (CBIII).

OS Centruroides sculpturatus (Bark scorpion).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;

OC Butihida; Buthoidea; Butihidae; Centruroides.

NCBI_TaxID=218467;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=93162874; PubMed=1286943;

RA Pete M.J., Conlon J.M., Murphy R.P.;

"Isolation and primary structure of a potent toxin from the venom of the scorpion *Centruroides sculpturatus* Ewing.";
Int. J. Pept. Protein Res. 40:582-585(1992).
CC -!- FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- TOXIC DOSE: LD(50) is 87 mg/kg by subcutaneous injection in mouse.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family. Beta-toxin subfamily.

DR HSSP; P01495; 1CN2.
DR InterPro; IPR001219; Neurotoxin.

DR InterPro; IPR002031; Scorpion_toxinL.

DR Pfam; PFO0537; Toxin_3_1.

DR PRINTS; PR00285; SCORPTOXIN.

DR PRODOM; PD000908; Scorpion_toxinL.

DR Direct protein sequencing; Ionic channel inhibitor; Toxin.

KW Direct protein sequencing; Ionic channel inhibitor; Neurotoxin;

KW Sodium channel inhibitor; Toxin.

FT DISULFID 12 64 By similarity.

FT DISULFID 16 40 By similarity.

FT DISULFID 25 45 By similarity.

FT DISULFID 29 47 By similarity.

SEQUENCE 65 AA; 7550 MW; 56BDA31F17D3C9 CRC64;

Query Match Best Local Similarity 50.0%; Pred. No. 2.3e-06; Length 65; Matches 21; Conservative 6; Mismatches 14; Indels 1; Gaps 1;

QY 16 YLCAPLGNDPDCIKIC-QKHGVDGYCYAFOCMCEPLKDENV 56

Db 14 YECURGLGNDYCARECQGSKSGCYAFACTHLEQQAV 55

Query Match Best Local Similarity 50.0%; Pred. No. 2.3e-06; Length 65; Matches 21; Conservative 6; Mismatches 14; Indels 1; Gaps 1;

QY 16 YLCAPLGNDPDCIKIC-QKHGVDGYCYAFOCMCEPLKDENV 56

Db 14 YECURGLGNDYCARECQGSKSGCYAFACTHLEQQAV 55

RESULT 6

0674Y8 PRELIMINARY; PRT; 64 AA.

AC Q674Y8; ID Q674Y8;

DR 05-JUL-2004 (TrEMBLrel. 27. Created)

DR 05-JUL-2004 (TrEMBLrel. 27. Last sequence update)

DR Beta-toxin (Fragment).

OS Centruroides noxius (Mexican scorpion).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; scorpiones;

OC Buthidae; Buthoidea; Buthidae; Centruroides sculpturatus Ewing.

OC NCBI_TAXID=6878;

RN [1]

SEQUENCE FROM N.A.

RA Zhi S.; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

RL -!- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

DR AV351302; AAR08037.1; -.

DR HSSP; P01493; 1UZA.

DR GO; GO:0005576; C: extracellular; IBA.

DR GO; GO:0008220; F: ion channel inhibitor activity; IBA.

DR GO; GO:0006932; P: defense response; IBA.

DR GO; GO:0009405; P: pathogenesis; IBA.

DR InterPro; IPR003614; Knot1.

DR InterPro; IPR002061; Scorpion_toxinL.

DR Pfam; PF00537; Toxin_3_1.

DR PRINTS; PR00285; SCORPTOXIN.

DR SMART; SM00505; Knot1; 1.

FT NON_TER 1 1

SEQUENCE 64 AA; 6929 MW; 8300977935D08A91 CRC64;

Query Match Best Local Similarity 41.8%; Pred. No. 4.4e-06; Length 64; Matches 23; Conservative 5; Mismatches 19; Indels 2; Gaps 1;

QY 34.1%; PRT; 64 AA.

Db 41 1

Query Match Best Local Similarity 46.9%; Pred. No. 4.4e-06; Length 64; Matches 23; Conservative 5; Mismatches 19; Indels 2; Gaps 1;

QY 34.1%; PRT; 64 AA.

Db 19 1

Query Match Best Local Similarity 46.9%; Pred. No. 4.4e-06; Length 64; Matches 23; Conservative 5; Mismatches 19; Indels 2; Gaps 1;

QY 34.1%; PRT; 64 AA.

Db 19 1

"Isolation and primary structure of a potent toxin from the venom of the scorpion *Centruroides sculpturatus* Ewing.";

Int. J. Pept. Protein Res. 40:582-585(1992).
CC -!- FUNCTION: Binds to sodium channels and inhibits the inactivation

of the activated channels, thereby blocking neuronal transmission.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family. Beta-toxin subfamily.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

"Isolation and primary structure of a potent toxin from the venom of the scorpion *Centruroides sculpturatus* Ewing.";

Int. J. Pept. Protein Res. 40:582-585(1992).
CC -!- FUNCTION: Binds to sodium channels and inhibits the inactivation

of the activated channels, thereby blocking neuronal transmission.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

"Isolation and primary structure of a potent toxin from the venom of the scorpion *Centruroides sculpturatus* Ewing.";

Int. J. Pept. Protein Res. 40:582-585(1992).
CC -!- FUNCTION: Binds to sodium channels and inhibits the inactivation

of the activated channels, thereby blocking neuronal transmission.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the venom gland.

CC -!- TISSUE SPECIFICITY: Expressed by the alpha/beta-scorpion toxin family.

CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

CC -!- HIGHLY POTENT.

CC -!- SUBCELLULAR LOCATION: Expressed by the

OX NCBI_TaxID=218467;
 RN [1] SEQUENCE FROM N.A.
 RA Zhu S.;
 RP Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 RL SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -| SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.
 DR EML; AY351306; AAR08041.1; -.
 DR HSSP; P01493; 1JZA.
 DR GO:0005576; C:extracellular; IBA.
 DR GO:0008200; F:ion channel inhibitor activity; IBA.
 DR GO:0005515; F:protein binding; IBA.
 DR GO:0006932; P:defense response; IBA.
 DR GO:0009405; P:pathogenesis; IBA.
 DR InterPro; IPR03614; Knot1.
 DR InterPro; IPR001219; Neurotoxin.
 DR InterPro; IPR02061; Scorpion_toxinL.
 DR PFam; PF00537; Toxin 3; 1.
 DR PRINTS; PR00285; SCORPTOXIN.
 DR PfDom; PD006908; TOXIN.
 DR SMART; SM00205; Knot1; 1.
 DR NON_TER 64 64
 SQ SEQUENCE 64 AA; 7137 MW; 8EBEFD8934D78C47 CRC64;
 Query Match 33.8%; Score 116; DB 2; Length 64;
 Best Local Similarity 46.9%; Pred. No. 5.7e-06;
 Matches 23; Conservative 4; Mismatches 20; Indels 2; Gaps 1;

RESULT 9
 ID Q6V4Y0 PRELIMINARY; PRT; 64 AA.
 AC Q6V4Y0;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DR 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DR 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Beta-toxin (Fragment).
 OS Centruroides noxius (Mexican scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Buthidae; Buthoidea; Centruroides.
 OX NCBI_TaxID=6677;
 RN [1] SEQUENCE FROM N.A.
 RA Zhu S.;
 RP Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 CC -| SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.
 DR EML; AY351310; 1JZA.
 DR GO:0005576; C:extracellular; IBA.
 DR GO:0008200; F:ion channel inhibitor activity; IBA.
 DR GO:0006932; P:defense response; IBA.
 DR GO:0009405; P:pathogenesis; IBA.
 DR InterPro; IPR003614; Knot1.
 DR InterPro; IPR001219; Neurotoxin.
 DR PRINTS; PR00285; SCORPTOXIN.
 DR PfDom; PD006908; TOXIN.
 DR SMART; SM00205; Knot1; 1.
 DR NON_TER 64 64
 SQ SEQUENCE 64 AA; 7382 MW; 01A24DFF96C24FCC8 CRC64;
 Query Match 33.8%; Score 116; DB 2; Length 64;
 Best Local Similarity 42.3%; Pred. No. 5.7e-06;
 Matches 22; Conservative 10; Mismatches 18; Indels 2; Gaps 2;

RESULT 10
 ID Q6V4Y4 PRELIMINARY; PRT; 64 AA.
 AC Q6V4Y4;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DE Beta-toxin (Fragment).
 OS Centruroides sculpturatus (Bark scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Buthidae; Buthoidea; Centruroides.

PT NON TER 1 7549 MW; 97559FF9BF84F36 CRC64;
 SQ SEQUENCE 66 AA; 1
 Query Match 32.9%; Score 113; DB 2; Length 66;
 Best Local Similarity 55.9%; Pred. No. 1.3e-05;
 Matches 18; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
 Qy 16 YLCAPLGNPDCIKIKQKHGVGDYGYCAEQCWE 49
 Db 14 YSCWILGENEYCTAECCKETGAGVGYCHGFGCWCE 47

RESULT 15

Q68PG7 PRELIMINARY; PRT; 67 AA.
 ID Q68PG7
 AC
 DR 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE CexB neurotoxin (Fragment).
 GN Name=CexB;
 OS Centruroides exilicauda (Bark scorpion).
 OC Buthidae; Arthropoda; Chelicerata; Arachnida; Scorpiones
 OC Buthidae; Buthidae; Centruroides.
 NCBI_TAXID=6879;
 RN [1]
 RP
 SEQUENCE FROM N.A.

RA Valdez-Cruz N.A.; Davila S.; Licea A.; Corona M.; Zamudio F.Z.,
 RA Garcia-Valdes J.; Boyer L.; Possani L.D.;
 RT "Biochemical, genetic and physiological characterization of venom
 components from two species of scorpions: Centruroides exilicauda Wood
 and Centruroides Ewing.",
 RL Biochimie 0:0 (2004).

CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family.

DR AY649866; AAT9799.1;
 DR GO:0009405; P:Pathogenesis; IEA.
 DR InterPro; IPR003614; Knot1.
 DR InterPro; IPR001219; Neurotoxin.
 DR InterPro; IPR00261; Scorpion_toxinL.
 DR PFAM; PF00537; Toxin_3.1.
 DR PRINTS; PR00285; SCORPNTOXIN.
 DR PRINTS; PR00284; TOXIN.
 DR ProDom; PD000908; Scorpion_toxinL_1.
 DR SMART; SM00505; Scorpion_toxinL_1.
 KW Neurotoxin.
 PT NON TER 1 1
 SQ SEQUENCE 67 AA; 1
 Query Match 32.9%; Score 113; DB 2; Length 67;
 Best Local Similarity 52.9%; Pred. No. 1.3e-05;
 Matches 18; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
 Qy 16 YLCAPLGNPDCIKIKQKHGVGDYGYCAEQCWE 49
 Db 15 YSCWILGENEYCTAECCKETGAGVGYCHGFGCWCE 48

Search completed: July 8, 2005, 15:33:03
 Job time : 179 secs

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OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 17:12:09 ; Search time 84.5225 Seconds
 (without alignments)
 3426.556 Million cell updates/sec

Title: US-10-617-978-17_COPY_73_249
 Perfect score: 177
 Sequence: 1 gccgacgtggccaggaaacta.....acgaaaacgtcaagggtgtga 177

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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 2: /cgn2_6/pododata/1/ina/5B_COMB.seq:
 3: /cgn2_6/pododata/1/ina/5A_COMB.seq:
 4: /cgn2_6/pododata/1/ina/5B_COMB.seq:
 5: /cgn2_6/pododata/1/ina/PECTUS_COMB.seq:
 6: /cgn2_6/pododata/1/ina/backfiles1.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description	
1	41.6	23.5	723	4	US-10-152-296-1		Sequence 1, Appli	
2	40	22.6	285	1	US-08-435-040-1		Sequence 1, Appli	
3	40	22.6	285	3	US-09-020-216-1		Sequence 1, Appli	
4	39	22.0	2634	3	US-08-941-336-1		Sequence 1, Appli	
5	38.6	21.8	615	4	US-09-902-540-6862		Sequence 68/2, Appli	
c	6	38.6	21.8	618	4	US-09-902-540-58		Sequence 58, Appli
7	38.2	21.6	1849	2	US-08-676-166A-1		Sequence 1, Appli	
8	37.8	21.5	197	4	US-08-472-053-43		Sequence 43, Appli	
9	37.2	21.0	1269	1	US-08-265-429A-4		Sequence 1, Appli	
10	37.2	21.0	1269	4	PCT-US95-01069-4		Sequence 4, Appli	
11	37.2	21.0	3404	1	US-08-265-429A-1		Sequence 1, Appli	
12	37.2	21.0	3404	5	PCT-US95-01069-1		Sequence 1, Appli	
13	37.2	21.0	3503	4	US-09-373-212-2		Sequence 2, Appli	
14	36.6	20.7	394	3	US-08-866-140-22		Sequence 22, Appli	
15	36.6	20.7	394	3	US-09-103-875-28		Sequence 28, Appli	
16	35.8	20.2	1266	4	US-09-252-991A-1008		Sequence 100/8, Appli	
17	35.6	20.1	426	4	US-09-252-991A-10269		Sequence 102/69, Appli	
18	35.6	20.1	642	4	US-09-152-991A-10480		Sequence 104/80, Appli	
c	35.6	20.1	1272	4	US-09-252-991A-10690		Sequence 106/90, Appli	
c	35.4	20.0	1080	4	US-09-902-540-9563		Sequence 95/63, Appli	
c	35.4	20.0	14823	4	US-09-502-540-10087		Sequence 108/07, Appli	
22	35.2	19.9	477	2	US-08-670-186-3		Sequence 3, Appli	
23	35.2	19.9	477	2	US-08-670-186-5		Sequence 5, Appli	
24	35.2	19.9	950	4	US-09-640-211A-156		Sequence 156, Appli	
25	35	19.8	50937	3	US-09-428-517-1		Sequence 1, Appli	
26	34.8	19.7	1752	3	US-09-360-779-1		Sequence 1, Appli	
27	34.8	19.7	1752	3	US-09-435-335-1		Sequence 1, Appli	

RESULT 1
 US-10-152-296-1
 ; Sequence 1, Application US/10152296
 ; Patent No. 6723557
 ; GENERAL INFORMATION:
 ; APPLICANT: Peelle, Beau
 ; Rigel Pharmaceuticals, Incorporated
 ; TITLE OF INVENTION: Incorporated Evolution of Protein in Mammalian Cells
 ; FILE REFERENCE: 02104-000110US
 ; CURRENT APPLICATION NUMBER: US 10/152,296
 ; CURRENT FILING DATE: 2002-12-10
 ; PRIORITY APPLICATION NUMBER: US 60/291,871
 ; PRIORITY FILING DATE: 2001-05-18
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 1
 ; LENGTH: 723
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:mammalian Sequence:mouse protein (DsRed) of Discosoma sp.
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(723)
 ; OTHER INFORMATION: "red" red Fluorescent protein (RFP)
 ; OTHER INFORMATION: "red"
 ; OTHER INFORMATION: DsRed
 US-10-152-296-1

Query Match 23.5%; Score 41.6; DB 4; Length 723;
 Best Local Similarity 53.0%; Pred. No. 0.011; Missmatches 0; Indels 0; Gaps 0;

Query Match 2 CGAGGTGCCAGGGAACTACCCGCTGGACACCTACCTGCGCACCC 61
 Best Local Similarity 53.0%; Pred. No. 0.011; Missmatches 0; Indels 0; Gaps 0;

Query Match 209 CCAAGCTTACAGTGAAGCAGCCGGAGATCCCGACTACAGAGCTTCCTTCCTCC 268

Query Match 62 TGGGGACACCCGAACTGCATCAAGATCTGCCAGAACGAGCGCTCGACTACGGCTACT 121

Query Match 269 AGGGCTTCAAGTGGAGCGCGGTGATGAACTTCGAGACGGCGCTGGTGAACCC 328

Query Match 122 GCTAGCGTTCCAGTGGTGGAGCTTCCTGAAAGCAGGAACTCTCA 169

Query Match 329 AGGACTCTCCCTGAGGACGGCTCTCATCTACAAGGTGAAGTCA 376

RESULT 2
 US-08-435-040-1
 ; Sequence 1, Application US/08435040
 ; Patent No. 5756340

GENERAL INFORMATION

APPLICANT: Hammock, Bruce D.

APPLICANT: Herrmann, Rafael.

TITLE OF INVENTION: Insect Control With Multiple Toxins

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Majestic, Parsons, Siebert & Hsue
STREET: Four Embarcadero Center, Suite 1450
CITY: San Francisco
STATE: California
COUNTRY: U.S.A.
ZIP: 94111-4121

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/435,040

FILING DATE: 08-MAY-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Siebert, J. Suzanne

REGISTRATION NUMBER: 28,758

REFERENCE/DOCKET NUMBER: 2500.078US0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 362-5556

TELEX: 278638 MGPS

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 285 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-435-040-1

Query Match 22.6%; Score 40; DB 1; Length 285;

Best Local Similarity 61.5%; Pred. No. 0.023; Indels 0; Gaps 0;

Matches 64; Conservative 0; Mismatches 40; DelIns 0; Gaps 0;

RESULT 4 US-08-941-936-1

; Sequence 1, Application US/08941936

; Patent No. 6054305

; GENERAL INFORMATION:

; APPLICANT: Tatsumi, Hiroki

; APPLICANT: Eisaki, Naoki

; APPLICANT: Horieuchi, Tatsuo

; APPLICANT: Nagahara, Ayumu

; TITLE OF INVENTION: Pyruvate Orthophosphate Dikinase Gene,

; TITLE OF INVENTION: Recombinant DNA, and Process For Producing Pyruvate

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MEDLEN & CARROLL, LLP

; STREET: 220 Montgomery Street, Suite 2200

; CITY: San Francisco

; STATE: CA

; COUNTRY: US

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/941,936

; FILING DATE: 01-OCT-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Carroll, Peter G.

; MEDIUM TYPE: Floppy disk

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/941,936

; FILING DATE: 01-OCT-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Carroll, Peter G.

REGISTRATION NUMBER: 32,837
 REFERENCE/DOCKET NUMBER: HIRAKI-030009
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-705-8110
 TELEFAX: 415-397-8338
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2634 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: Microbispora thermotrosea
 STRAIN: IFO 14047
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..2634
 US-08-941-936-1

Query Match 22.0%; Score 39; DB 3; Length 2634;
 Best Local Similarity 58.0%; Pred. No. 0.089; Indels 0; Gaps 0;
 Matches 69; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 39 CAACACTTACCTGTGGCAACCCCTGGGACAACCGGAAGTCATGCCAGAA 98
 Db 2475 CAAGCTCGCATCTGGGAGCACGGGGACCCGACTGGTGTGGTCTGCCAGA 2534

Qy 99 GCACCGCGTGCAGTACGGGTTACTGCTAACGGGTTCCAGTGTGGTGGAGAAGG 157
 Db 2535 GATGCCCTCGACTAACGTCTCTGCTGCCATTCCGGCATTCGGCGCTGGGG 2593

RESULT 5
 US-09-902-540-6862
 Sequence 6862, Application US/09902540
 / Patent No. 6833447
 GENERAL INFORMATION:
 APPLICANT: Goldman, Barry S.
 APPLICANT: Hinkie, Gregory J.
 APPLICANT: Slater, Steven C.
 APPLICANT: Wiegand, Roger C.
 TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 FILE REFERENCE: 38-10 (15849) B
 CURRENT APPLICATION NUMBER: US/09/902,540
 CURRENT FILING DATE: 2001-07-10
 PRIOR APPLICATION NUMBER: 60/217,883
 PRIOR FILING DATE: 2000-07-10
 SEQ ID NO 6862
 LENGTH: 615
 TYPE: DNA
 ORGANISM: Myxococcus xanthus
 US-09-902-540-6862

Query Match 21.8%; Score 38.6; DB 4; Length 615;
 Best Local Similarity 52.9%; Pred. No. 0.075; Indels 0; Gaps 0;
 Matches 83; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 13 GGAACTTACCCGCTGGACAGCTGGAAACAAACACTTACCTGTGGCAAC 72
 Db 178B GGAAAGCTGGCACCAGAACCCGAAACGATTCGGGACATGCCGAGTCAC 237

Qy 73 CGGGACTGCAAGTCAAGTGGCAGAGCAAGGAGTACTCTAACCGTTC 132
 Db 238 GAATGCACATGGGATTGGCCAGTGTGGGGTCACTGGCGAGGCCAACAGTAC 297

Qy 133 CAGTGTGGTGAGTCTGAAGGAGGAGAACGCTCA 169
 Db 298 AACGGCTTCGCCAGTGTGGAGATGACCCA 334

RESULT 7
 US-08-676-166A-1
 Sequence 1, Application US/08676166A
 / Patent No. 5955270
 GENERAL INFORMATION:
 APPLICANT: Radford, Alan
 APPLICANT: Parish, John H.
 TITLE OF INVENTION: EXPLOITATION OF THE CELLULASE COMPLEX OF
 NEUROSPORA
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/676,166A
 FILING DATE: 15-JUL-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1321-1-002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-341-1684
 INFORMATION FOR SEQ ID NO: 1:

```

SEQUENCE CHARACTERISTICS:
LENGTH: 1849 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
IMMEDIATE SOURCE:
TOPOLOGY: linear
LIBRARY: lambda J1
CLONE: X

FEATURE:
NAME/KEY: CDS
LOCATION: join(152..832, 892..1758)
FEATURE:
NAME/KEY: intron
LOCATION: 833..891
FEATURE:
NAME/KEY: exon
LOCATION: <152..832
FEATURE:
NAME/KEY: exon
LOCATION: 892..>1761
PUBLICATION INFORMATION:
AUTHORS: Taleb, F
TITLE: Cloning Sequencing and homologies of the
TITLE: CBH-1 (exocellulobiohydrolase) gene of Neurospora
TITLE: crassa
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 1849

Query Match 21.6%; Score 38.2; DB 2; Length 1849;
Best Local Similarity 52.9%; Pred. No. 0.14; 0; Gaps 0;
Matches 82; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Query Match 21.5%; Score 38.4; DB 4; Length 197;
Best Local Similarity 61.4%; Pred. No. 0.079; 0; Gaps 1;
Matches 81; Conservative 0; Mismatches 45; Indels 6; Gaps 1;
Organism: Leuirus quinquestriatus hebraeus
US-08-472-053-43

Qy 39 CAACACCTACCTGTCGCCACCCCTGGGACACTCGATCAAGATCTGCCAGAA 98
Db 29 CGACGGGGCAAGGTGGTTGCCTGATGGCACGAGGTGTCAGGGC 88
Qy 99 GCACGGGGTGTGACTACCGCTACTGTACCGCTACTGCTGGGCTGGGCT 152
Db 89 TTACGGGGCAGCTACCGCTACTGCTGGGCTGGGCTGGGCTGGGCT 148
Qy 153 GAAGGAGGAGAA 164
Db 149 GCGGGACAA 160

RESULT 9
US-08-265-429A-4
Sequence 4, Application US/08265429A
Patent No. 5671151
GENERAL INFORMATION:
APPLICANT: Wilson, David B.
APPLICANT: Walker, Larry P.
APPLICANT: Zhang, Sheng
TITLE OF INVENTION: Thermostable Cellulase From A Thermomonospora Gene
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hodges, Russ, Andrews, Woods & Goodyear
STREET: 1800 One M&T Plaza
CITY: Buffalo
STATE: New York
COUNTRY: United States
ZIP: 14203-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
SOFTWARE: Wordperfect for Windows 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,429A
FILING DATE: 24/06/94
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, M. Bud
REGISTRATION NUMBER: 35,300
REFERENCE/DOCENT NUMBER: 18617.0008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 856-4000
TELEFAX: 716-849-0349
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1269 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double-stranded
TOPOLOGY: Linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Thermomonospora fusca
STRAIN: YX36
CELL TYPE: bacterium
US-08-265-429A-4

RESULT 8
US-08-472-053-43
Sequence 43, Application US/08472053
PATENT NO. 6689356
GENERAL INFORMATION:
APPLICANT: ZLOTKIN, ELIAHU
APPLICANT: MAEDA, SUSUMU
APPLICANT: MCCUTCHEON, BILLY F.
APPLICANT: HAMMOCK, BRUCE D.
APPLICANT: FOWLER, ELIZABETH
APPLICANT: BELAJADE, RANA M.
TITLE OF INVENTION: RECOMBINANT BACULOVIRUSES PRODUCING
TITLE OF INVENTION: INSECT TOXINS
FILE REFERENCE: UC058.1FWCP2
CURRENT APPLICATION NUMBER: US/08/472,053
CURRENT FILING DATE: 2004-11-13
PRIOR APPLICATION NUMBER: 08/229417
PRIOR FILING DATE: 1994-04-15
PRIOR APPLICATION NUMBER: 07/629603
PRIOR FILING DATE: 1990-12-19
PRIOR APPLICATION NUMBER: 07/286087
PRIOR FILING DATE: 1988-12-19
NUMBER OF SEQ ID NOS: 49
NUMBER OF SEQ ID NOS: 49
Best Local Similarity 50.4%; Pred. No. 0.24;
Matches 63; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
Query Match 21.0%; Score 37.2; DB 1; Length 1269;

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Qy 64 GGGGACAACCGGACTGATCAAGATCTGCCAGAGCACGGCTGACTAACGGTACTGC 123
 Db 454 GGGGACAACCGGACTGATCAAGATCTGCCAGAGCACGGCTGACTAACGGTACTGC 513

Qy 124 TAGCGTTCCAGTGTGGCTGGAGTCTCTGAAGGCGGAAGCGTA 169
 Db 514 TAGGCCCTCCGAAGCTGGGAGATCCGAACGCTCAACTACA 559

RESULT 10
 PCT-US95-09069-4
 / Sequence 4, Application PC/TUSS509069
 / GENERAL INFORMATION:
 / APPLICANT: Wilson, David B.
 / APPLICANT: Walker, Larry P.
 / APPLICANT: Zhang, Sheng
 / TITLE OF INVENTION: Thermostable Cellulase From A Thermomonospora Gene
 / NUMBER OF SEQUENCES: 8
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Hodges, Russ, Andrews, Woods & Goodyear
 / STREET: 1800 One M&T Plaza
 / CITY: Buffalo
 / STATE: New York
 / COUNTRY: United States
 / ZIP: 14203-2391
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
 / COMPUTER: IBM compatible
 / OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
 / SOFTWARE: Wordperfect for Windows 5.1
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/265,429A
 / FILING DATE: 24/06/94
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Nelson, M. Bud
 / REGISTRATION NUMBER: 35,300
 / REFERENCE/DOCKET NUMBER: 18617-0008
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (716)856-4000
 / TELEFAX: 716-842-0319
 / INFORMATION FOR SEQ ID NO: 1:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 3404 nucleotides
 / TYPE: nucleic acid
 / STRANDEDNESS: double-stranded
 / TOPOLOGY: linear
 / MOLECULE TYPE: Genomic DNA
 / ORIGINAL SOURCE:
 / ORGANISM: Thermomonospora fusca
 / STRAIN: YX36
 / CELL TYPE: bacterium
 / US-08-265-429A-1

Qy 64 GGCAGCAACCCGGACTCAAGATCTGCCAGAGCACGGCTGACTAACGGTACTGC 123
 Db 454 GGCAGCAACCCGGACTCAAGATCTGCCAGAGCACGGCTGACTAACGGTACTGC 513

Qy 124 TAGCGTTCCAGTGTGGCTGGAGTCTCTGAAGGCGGAAGCGTA 169
 Db 514 TAGGCCCTCCGAAGCTGGGAGATCCGAACGCTCAACTACA 559

RESULT 11
 PCT-US95-09069-4
 / Sequence 5, Application US/08265429A
 / Patent No. 5677151
 / GENERAL INFORMATION:
 / APPLICANT: Wilson, David B.
 / APPLICANT: Walker, Larry P.
 / APPLICANT: Zhang, Sheng
 / TITLE OF INVENTION: Thermostable Cellulase From A Thermomonospora Gene
 / NUMBER OF SEQUENCES: 8
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Hodges, Russ, Andrews, Woods & Goodyear
 / STREET: 1800 One M&T Plaza
 / CITY: Buffalo
 / STATE: New York
 / COUNTRY: United States
 / ZIP: 14203-2391

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS / Microsoft Windows 3.1
 SOFTWARE: Wordperfect for Windows 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/09069
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: U.S. Serial No. 08/265,429
 FILING DATE: 24/06/94
 ATTORNEY /AGENT INFORMATION:
 NAME: Neilson, M. Bud
 REGISTRATION NUMBER: 35,300
 REFERENCE/DOCKET NUMBER: 18617.0008
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (716)856-4000
 TELEFAX: 716-849-0349
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3404 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: double-stranded
 TOPOLOGY: linear
 MOLECULE TYPE: Genomic DNA
 ORIGINAL SOURCE:
 ORGANISM: Thermomonospora fusca
 STRAIN: YX36
 CELL TYPE: bacterium
 PCT-US95-09069-1

Query Match 64 Score 37.2; DB 5; Length 3404;
 Best Local Similarity 59.4%; Pred. No. 0.32%; Indels 0; Gaps 0;
 Matches 63; Conservative 0; Mismatches 43;

Qy 64 GGGGACAACCCGGAAGTCAAGATTCGCCAGAGCAGGGCTACTCGC 123
 Db 1447 GGGGCAACGGAGCTGGCCCTAGTGAGGAGAACGGGGTACGTGTCGC 1506

Qy 124 TACCGGTTCACTGTTGGCGAGTCCCTGAAGGACGAAAGCTCA 169
 Db 1507 TACGCCCTCGCAAGCTGGCGAGATCCGAACSTCTAACACTACA 1552

RESULT 13
 US-09-373-272-2
 / Sequence 2, Application US/09373272
 / PATENT NO. 6818803
 / GENERAL INFORMATION:
 / APPLICANT: Austin-Phillips, Sandra
 / APPLICANT: Burgess, Richard D
 / APPLICANT: German, Thomas L
 / APPLICANT: Ziegelhofer, Thomas
 TITLE OF INVENTION: Transgenic Plants as an Alternative Source of
 Lignocellulosic-Degrading Enzymes
 FILE REFERENCE: Transgenic Plants Expressing Cellulase
 CURRENT FILING DATE: 1999-08-12
 EARLIER FILING DATE: 1997-06-26
 NUMBER OF SEQ ID NOS: 32
 SEQ ID NO 2
 LENGTH: 3503
 TYPE: DNA
 ORGANISM: Thermomonospora fusca
 US-09-373-272-2

Query Match 64 Score 37.2; DB 4; Length 3503;
 Best Local Similarity 59.4%; Pred. No. 0.32%; Indels 0; Gaps 0;
 Matches 63; Conservative 0; Mismatches 43;

Qy 64 GGGGACAACCCGGAAGTCAAGATTCGCCAGAGCAGGGCTACTCGC 123
 Db 1507 TACGCCCTCGCAAGCTGGCGAGATCCGAACSTCTAACACTACA 1552

RESULT 14
 US-08-866-340-22
 / Sequence 22, Application US/08866340
 / Patent No. 6000318
 / GENERAL INFORMATION:
 / APPLICANT: Szy, Moshe
 / APPLICANT: Biger, Pascal
 / APPLICANT: Ramchandani, Shyam
 / TITLE OF INVENTION: DNA MBTHYLTRANSFERASE GENOMIC
 / TITLE OF INVENTION: SEQUENCES AND ANTISENSE OLIGONUCLEOTIDES
 / NUMBER OF SEQUENCES: 64
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: HALF AND DOOR LLP
 / STREET: 60 State Street
 / CITY: Boston
 / STATE: MA
 / COUNTRY: United States of America
 / ZIP: 02109
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patent In Release #1.0, Version #1.30
 / CURRENT APPLICATION NUMBER: US/08/866,340
 / APPLICATION NUMBER: US/08/866,340
 / FILING DATE:
 / CLASSIFICATION: 536
 / ATTORNEY /AGENT INFORMATION:
 / NAME: Keown, Wayne A.
 / REGISTRATION NUMBER: 33,923
 / REFERENCE DOCKET NUMBER: 106-101-187
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (617) 526-6000
 / TELEFAX: (617) 526-5000
 / INFORMATION FOR SEQ ID NO: 22:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 394 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: both
 / TOPOLOGY: linear
 / MOLECULE TYPE: Other nucleic acid
 / HYPOTHETICAL: NO
 / ANTI-SENSE: NO
 / -US-08-866-340-22

Query Match 64 Score 36.6; DB 3; Length 394;
 Best Local Similarity 53.1%; Pred. No. 0.25%;
 Matches 78; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
 Qy 64 GGGGACAACCCGGAAGTCAAGATTCGCCAGAGCAGGGCTACTCGC 123
 Db 37 CAGCCCTGAGAACCCCAAGTCCCACTCCAGGAGTACCGAATCAGCT 96
 Qy 90 CTGGCAAGAGCAGCGGCTGACTACGGCTACTCGTACGGTTCAGCTGGAGTT 149
 Db 97 CTACTGGGGAGGAGGAGGCTGGGACTCAAGGCTGTGAGGACGCCACCGT 156

Query Match 64 Score 36.6; DB 3; Length 394;
 Best Local Similarity 53.1%; Pred. No. 0.25%;
 Matches 78; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
 Qy 64 GGGGACAACCCGGAAGTCAAGATTCGCCAGAGCAGGGCTACTCGC 123
 Db 37 CAGCCCTGAGAACCCCAAGTCCCACTCCAGGAGTACCGAATCAGCT 96
 Qy 90 CTGGCAAGAGCAGCGGCTGACTACGGCTACTCGTACGGTTCAGCTGGAGTT 149
 Db 97 CTACTGGGGAGGAGGAGGCTGGGACTCAAGGCTGTGAGGACGCCACCGT 156

RESULT 15
 US-09-103-875-28
 / Sequence 15, Application US-09-103-875-28

Sequence 28, Application US/09103875A
Patent No. 6221849
GENERAL INFORMATION:
APPLICANT: SZYF, Moshe
APPLICANT: Bigey, Pascal
APPLICANT: Ramchandani, Shyam
TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC SEQUENCES AND ANTISENSE OLIGONUCLEOTIDES
FILE REFERENCE: 106101.194
CURRENT APPLICATION NUMBER: US/09/103,875A
CURRENT FILING DATE: 1998-06-24
EARLIER APPLICATION NUMBER: 60/069,865
EARLIER FILING DATE: 1997-12-17
EARLIER APPLICATION NUMBER: 08/866,340
EARLIER FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 28
LENGTH: 394
TYPE: DNA
ORGANISM: Homo sapiens
US-09-103-875-28

Query Match 20.7%; Score 36.6; DB 3; Length 394;
Best Local Similarity 53.1%; Pred. No. 0.25;
Matches 78; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
Qy 30 CAGCTGGACACCTTACCTGTGGCAACCCCTGGGAAACCGGAATGCAATCAAGAT 89
Db 37 CAGGCCCTGAGAACCCACAAAGTCACACTAGCAGCTAACACGCAATCAACCTGCT 96
Qy 90 CTGCCAGAAGCACGGCGTGCAGTACGGTACTGCTACGCTTCCAGTGTGGCGAGTT 149
Db 97 CTACCTGGCGAGGAGCAAGGAGCAAGGTCAAGGTGTGACTTCAGGCTGTGACCGT 156
Qy 150 CCTGAGGGAGGAGGAGAACGTCAGGTGTG 176
Db 157 GGAGPATGGGAGGACCTGGCCGACTG 183

Search completed: July 30, 2005, 20:19:26
Job time : 100.522 secs

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			Adl35208 Plasmid p
			Ade24111 Proviral
			Aca55359 Transform
			Adr30815 Zebrafish
			Adr30814 Zebrafish
			Adq91222 Expression
			Ado09979 pBdT(dHSP)
			Adl135211 Plasmid p
			Ado56664 Plasmid p
			Ado4104 Vector pD
			Ado4113 Vector pT
			Adm82791 DNA repair
			Adm82792 DNA repair
			Ado4104 Vector pT
			Ado0962 Montabstra
			Ado66256 Corn seed
			Adj44616 Plant CDNA
			Adj42608 Synthetic
			Adc24132 Discosoma
			Adl14628 Discosoma
			Adl146211 Discosoma
			Aas78582 DNA encod
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effect score:	177		
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scoring table:	IDENTITY_NUC		
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searched:	4390206 seqs, 2959870667 residues		
total number of hits satisfying chosen parameters:	8780412		
minimum DB seq length:	0		
maximum DB seq length:	2000000000		
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	41.6	23.5	7508 13 Adr30814
	41.6	23.5	7616 13 Ado91222
	41.6	23.5	7910 4 Ado09979
	41.6	23.5	7927 12 Adl35211
	41.6	23.5	9320 6 Ado56664
	41.6	23.5	9658 12 Ado4104
	41.6	23.5	9678 12 Adl04103
	41.6	23.5	9731 11 Adm82791
	41.6	23.5	9782 11 ADMB2792
	41.6	23.5	10463 12 Adl04102
	41	23.2	726 10 Adh00962
	40.4	22.8	7 Ado66256
	40.4	22.8	714 12 ADJ44616
	40	22.6	285 2 AAT42608
	40	22.6	678 10 ADC24132
	40	22.6	678 11 ADL46282
	40	22.6	678 11 ADL46211
	39.8	22.5	AAS78582 5
	39.8	22.5	3128 5 AAT59458 4

ALGEMEEN

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  7: geneseqn200bs:*
  8: geneseqn200as:*
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 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*

RESULT 1
AD46281
ID AD46281 standard; DNA; 675 BP.
XX
AC AD46281;
XX
DT 27-DEC-2002 (first entry)
XX
DE Discosoma sp. drFP583 (NFP-6) mutant DNA, E57-NA.
XX
KW Fluorescent protein; chromoprotein; protease cleavage assay; filter;
KW fluorescence activated cell sorting application; fluorescent timer;
KW biosensor; fluorescence resonance energy transfer application; FRET;
KW colouring agent; recombinant DNA application; analyse detection assay;
KW barcode; barcode reader; barcode scanner; barcode analysis; barcode distribution;
KW barcode system; barcode recognition; barcode reading; barcode processing;
KW barcode management; barcode tracking; barcode tracking system;
KW barcode tracking software; barcode tracking application; barcode tracking
mutant; ds.
XX

```

SUMMARIES									
Result No.	Score	Query	Match	Length	DB	ID	Description	Location/Qualifiers	
1	41.6	AAD46281	Discosoma sp.	23.5	6	AAD46281	Discosoma	1. .675	
2	41.6	Aad46278	Discosoma	23.5	6	AAD46278	Discosoma	/*tag= ^a /product= "drf583 mutant protein, E57-NA"	
3	41.6	Aad46282	Discosoma	23.5	6	AAD46282	Discosoma	/note= "No stop codon"	
4	41.6	Aad28208	Discosoma	23.5	6	AAD28208	Discosoma	/partial	
5	41.6	Aad28207	Discosoma	23.5	6	AAD28207	Discosoma	WO200268459-A2.	
6	41.6	Aad28209	Discosoma	23.5	6	AAD28209	Discosoma	XX	
7	41.6	ADC24128	Discosoma	23.5	10	ADC24128	Discosoma	XX	
8	41.6	Ac146207	Discosoma	23.5	678	11	Ac146207	XX	06-SEP-2002.
9	41.6	Adc24134	Discosoma	23.5	681	10	ADC24134	XX	20-FEB-2002;
10	41.6	Ad146205	Human cod	23.5	681	11	AD146205	XX	0270983P.
11	41.6	Ad146225	Human cod	23.5	681	11	AD146225	XX	21-FEB-2001;
12	41.6	Aaa48743	Humanised	23.5	695	3	AAA48743	XX	04-DEC-2001;
13	41.6	Adn33980	Murat -Ev	23.5	704	11	Adn33980	XX	2001US-00006922.
14	41.6	Abz22476	Mammalian	23.5	723	8	ABZ22476	(CLON-) CLONTECH LAB INC.	
15	41.6	Adl18131	RFP-PS (NI	23.5	1638	10	ADL18131	XX	
16	41.6	Adl18155	RFP-PS (HI	23.5	1647	10	ADL18155	XX	
17	41.6	Adst75466	Fibrohexa	23.5	2721	13	ADST75466	XX	
18	41.6	Adst75468	Fibrohexa	23.5	2772	13	ADST75468	DR	
19	41.6	Adq91220	Mixed	23.5	4488	13	ADQ91220	WPI;	2002-691654/74.
20	41.6	Adq91220	Mixed	23.5	4502	5	ADQ91220	XX	P-PSDB; AAE28836.

OS Discosoma sp.
XX Key 1 Location/Qualifiers
FT CDS .678 /tag= a
FT /product= "Humanised wild-type Anthozoa protein drFP583"
XX PN WO200196373-A2.
XX PD 20-DEC-2001.
XX PP 13-JUN-2001; 2001WO-US019097.
XX PR 14-JUN-2000; 2000US-0211607P.
XX PA (CLON-) CLONTECH LAB INC.
XX PI Fradkov AF, Terstikh A;
XX DR WPI; 2002-154595/20.
XX DR P-NSDB; AAE17540.
XX PS Example 1; Fig 1; 89pp; English.
XX The invention relates to a fluorescent timer protein having an emission spectrum that changes over time after synthesis from a first wavelength to a second wavelength. The fluorescent timer proteins are useful in monitoring the activity of a promoter, determining the age of a protein, identifying an agent that modulates the activity of a promoter and in enriching a population of cells comprising a fluorescent timer protein. The fluorescent timer proteins are also useful for assessing gene expression during development of a multicellular organism or during cellular differentiation, in response to a drug or other inducer of promoter activity, as a reporter to serve as a read-out of promoter activity, monitoring intracellular protein movement or translocation, protein trafficking, or protein stability, to investigate temporal aspects of the activity of a regulatory element, for determining cell fate during development and organ remodelling in spatial and temporal visualisation of newly synthesised proteins and accumulated proteins, and in distinguishing between newly formed and pre-existing structures, e.g. membrane junctions and extracellular matrix components. The fluorescent timer proteins may further be used to investigate where photobleaching techniques are employed, as detectable labels, as selectable markers, as biosensors in prokaryotic and eukaryotic cells, in protease cleavage assays, and as second messenger detectors. The nucleic acids can be used to generate transgenic, non-human plants or animals or site-specific gene modifications in cell lines. The present sequence is a DNA encoding Discosoma sp. humanised wild-type Anthozoa protein drFP583 used for generating fluorescent proteins
XX Sequence 678 BP; 146 A; 223 C; 203 G; 106 T; 0 U; 0 Other;
Query Match 23.5%; Score 41.6; DB 6; Length 678;
Best Local Similarity 53.0%; Pred. No. 0.44;
Matches 89; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
Qy 2 CGGAGCTGCCAGGGAAACTACCCGGTAGCTGGAGACCTACCTGTGGCACCCC 61
Db 206 CCAAGGTGTAGTGTAGCCACCCCCCGAATCCCGACTAACAGAAGTGTCTTCGG 265
Qy 62 TGGCGGACACCCGACTCATAGATGTTGAGGAAGCCGGCCTCACTAGGTACT 121
Db 266 AGGGCTTCAGTGGAGCCGGTGTGAACCTTGAGGACGGGGTGTGACCGTGACCC 325
Qy 122 GCTPACGGCTTCCACTGTGTGCTGGAGCCGGACAGAACGTCGA 169
Db 326 AGGACTCTCCCTGAGGGACGGCTCATCTACAAGGTGCT 373

RESULT 6
AAD28209 ID AAD28209 standard; cDNA; 678 BP.
XX AC AAD28209;
XX DT 22-APR-2002 (first entry)
XX DE Discosoma sp. non-aggregating mutant timer protein E5NA encoding cDNA.
XX KW Fluorescent timer protein; protein movement; translocation; trafficking; promoter activity; gene expression; transgenic plant; Gene modification; protein age; mutant; E5NA; 68.
XX OS Discosoma sp.
XX FH Key 1: .678
XX CDS FT /*tag= a
XX PI Location/Qualifiers
XX DR /product= "Mutant E5NA protein"
XX PD 20-DEC-2001.
XX PF 13-JUN-2001; 2001WO-US019097.
XX PR 14-JUN-2000; 2000US-0211607P.
XX PA (CLON-) CLONTECH LAB INC.
XX PI Fradkov AF, Terstikh A;
XX DR WPI; 2002-154595/20.
XX DR P-NSDB; AAE17542.
XX PS New fluorescent timer proteins comprising an emission spectrum that changes over time from a first wavelength to a second wavelength, useful for monitoring intracellular protein movement, translocation, trafficking or stability.
XX PS Disclosure; Fig 3; 89pp; English.
XX The invention relates to a fluorescent timer protein having an emission spectrum that changes over time after synthesis from a first wavelength to a second wavelength. The fluorescent timer proteins are useful in monitoring the activity of a promoter, determining the age of a protein, identifying an agent that modulates the activity of a promoter and in enriching a population of cells comprising a fluorescent timer protein. The fluorescent timer proteins are also useful for assessing gene expression during development of a multicellular organism or during cellular differentiation, in response to a drug or other inducer of promoter activity, as a reporter to serve as a read-out of promoter activity, monitoring intracellular protein movement or translocation, protein trafficking, or protein stability, to investigate temporal aspects of the activity of a regulatory element, for determining cell fate during development and organ remodelling in spatial and temporal visualisation of newly synthesised proteins and accumulated proteins, and in distinguishing between newly formed and pre-existing structures, e.g. membrane junctions and extracellular matrix components. The fluorescent timer proteins may further be used to investigate where photobleaching techniques are employed, as detectable labels, as selectable markers, as biosensors in prokaryotic and eukaryotic cells, in protease cleavage assays, and as second messenger detectors. The nucleic acids can be used to generate transgenic, non-human plants or animals or site-specific gene modifications in cell lines. The present sequence is a DNA encoding Discosoma sp. E5NA non-aggregating fluorescent timer protein derived from fluorescent timer protein E5 by substituting amino acids at positions R2A, K5B and K9T. E5 protein is derived from humanised wild-type Anthozoa protein drFP583 by substituting Val at 105 and Ser to Thr at 197

SQ Sequence 678 BP; 145 A; 226 C; 203 G; 104 T; 0 U; 0 Other;
 Query Match 23.5%; Score 41.6; DB 6; Length 678;
 Best Local Similarity 53.0%; Pred. No. 0.44;
 Matches 89; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
 Qy 2 CCGACGTGGCAGGGACTACCGCTGGAAAGCTGACACCTACCGTGGCACCCC 61
 Db 206 CCAAAGTGTAGTGTAGTGAAACCCGGACTACAGTAGAACAGCTGGTCTTCGG 265
 Qy 62 TGGGGGACAAACCCGAGCTGATCAAGATCTGCCAGAAGGACGGCTCGAAGTACT 121
 Db 266 AGGGCTTCAGTGGGAGCGCTGTGATACTTCGAGGACCGGGCTGGACCGTGACC 325
 Qy 122 GCTACGGCTTCAGCTGGAGCTGGTGGCAAGGAGGAGAACTCA 169
 Db 326 AGGACTCTCCCTGCAGGGACGGCTCTCATCTACAAGGTGAAGTTCA 373

RESULT 7
 ADC24128 standard; DNA; 678 BP.

AC ADC24128;

DT 18-DEC-2003 (first entry)

XX Discosoma red fluorescent protein variant fast T1 DNA.

XX Discosoma red fluorescent protein; DsRed; AB interface; AC interface;
 KW fluorescence protein variant; transcription induction detection;
 KW fluorescence energy resonance transfer; FRET; protein kinase;
 KW protein phosphatase; ion indicator; ds; mutant; fast T1.

OS Synthetic.

OS Discosoma.

PN US2003059835-A1.

PD 27-MAR-2003.

PP 10-APR-2002; 2002US-00121258.

PR 26-FEB-2001; 2001US-00794308.

PR 24-MAY-2001; 2001US-00866538.

PA (TSIE/) TSIEN R Y.
 PA (CAMP/) CAMPBELL R E.

PI Tsien RY, Campbell RE;
 XX WPI; 2003-743764/70.

DR P-PSDB; ADC24129.

XX Novel polynucleotide sequence encoding Discosoma red fluorescent protein variant having a reduced propensity to oligomerize, useful for detecting transcriptional activity.

XX Example 1; SEQ ID NO 3: 67pp; English.

XX The invention describes a polynucleotide sequence (I) encoding a Discosoma red fluorescent protein (DsRed) variant having a reduced propensity to oligomerise, comprising amino acid substitutions at the AB and/or AC interfaces of the wild-type DsRed sequence (S1) comprising 225 amino acids, given in the specification, where the substitutions result in reduced propensity of the DsRed variant to form tetramers. (I) is useful for detecting transcriptional activity by providing a host cells containing a vector which comprises (I) operatively linked to an expression control sequence, and an unit to assay the variant fluorescent protein fluorescence, and assaying fluorescence of the variant fluorescent protein produced by (VII), where variant fluorescent protein fluorescence is indicative of transcriptional activity. A polynucleotide encoding a fusion protein is useful for the analysis of in vivo

CC localisation or trafficking of a polypeptide of interest. A polypeptide marker is useful as markers to identify the location and amount of a target protein produced, where the target protein is fused to the marker, as a complement to or alternative for the green fluorescent protein or its spectral variant for detecting induction of transcriptions in applications involving fluorescence energy resonance transfer (FRET), which detects events as the function of the movement of fluorescent donors and acceptors towards or away from each other, for making fluorescent sensors for protein kinase and phosphatase activities or indicators for ions and molecules such as Ca²⁺, Zn²⁺, for identifying the presence of a molecule in a sample, for identifying a specific interaction of a first and second molecule, for determining whether a sample contains an enzyme or for determining the pH of the sample. (I) is useful for identifying a region or condition that regulates the activity of an expression control sequence. This sequence encodes Discosoma red fluorescent protein variant fast T1.

SQ Sequence 678 BP; 141 A; 225 C; 205 G; 107 T; 0 U; 0 Other;
 Query Match 23.5%; Score 41.6; DB 10; Length 678;
 Best Local Similarity 53.0%; Pred. No. 0.44; ID 0; Gaps 0;
 Matches 89; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
 Qy 2 CCGACGTGGCAGGGACTACCGCTGGAAAGCTGACACCTACCGTGGCACCCC 61
 Db 206 CCARGGTGTACGTGAAGCACCCCGGACATCCCCGACTAACAGAGCTCCCTCCCG 265
 Qy 62 TGGGGACAAACCCGAGCTGATCAAGATCTGCCAGAAGGACGGCTCGAAGTACT 121
 Db 266 AGGGCTTCAGTGGAGGCGCTGTGAACTCTCGAGCAGGGCTGGTGAACCGTGACCC 325
 Qy 122 GCTACGGCTTCAGCTGGAGTGGTGGAGGAGGAGAACTCA 169
 Db 326 AGGACTCTCCCTGCAGGGACGGCTCTCATCTACAAGGTGAAGTTCA 373

XX Sequence 678 BP; 141 A; 225 C; 205 G; 107 T; 0 U; 0 Other;
 Query Match 23.5%; Score 41.6; DB 10; Length 678;
 Best Local Similarity 53.0%; Pred. No. 0.44; ID 0; Gaps 0;
 Matches 89; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
 Qy 2 CCGACGTGGCAGGGACTACCGCTGGAAAGCTGACACCTACCGTGGCACCCC 61
 Db 206 CCARGGTGTACGTGAAGCACCCCGGACATCCCCGACTAACAGAGCTCCCTCCCG 265
 Qy 62 TGGGGACAAACCCGAGCTGATCAAGATCTGCCAGAAGGACGGCTCGAAGTACT 121
 Db 266 AGGGCTTCAGTGGAGGCGCTGTGAACTCTCGAGCAGGGCTGGTGAACCGTGACCC 325
 Qy 122 GCTACGGCTTCAGCTGGAGTGGTGGAGGAGGAGAACTCA 169
 Db 326 AGGACTCTCCCTGCAGGGACGGCTCTCATCTACAAGGTGAAGTTCA 373

RESULT 8
 ADL46207
 ID ADL46207 standard; DNA; 678 BP.

AC ADL46207;

XX DT 20-MAY-2004 (first entry)

DB Discosoma red fluorescent protein (DsRed) variant T1 coding sequence.
 XX ds; gene; red fluorescent protein; DsRed; fluorescence; hybridization assay.
 KW oligomerization; tetramerization; immunoassay; hybridization assay.
 XX OS Discosoma sp.
 XX FN Key
 XX FT CDS 1..678
 XX FT /tag= "DsRed variant T1 protein"
 XX FT /product= "DsRed variant T1 protein"
 XX PN WO2003086446-A1.

XX XX 23-OCT-2003.
 XX PD XX
 XX PR 09-APR-2003; 2003NO-US010879.
 XX PR 10-APR-2002; 2002US-00121258.
 XX PR 29-JUL-2002; 2002US-00209208.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Tsien RY, Campbell RE, Baird GS;
 XX DR WPI; 2003-845265/78.
 XX DR P-PSDB; ADL46206.
 XX PT New monomeric and dimeric Anthozoan fluorescent protein variants with

reduced propensity to oligomerize, and encoding polynucleotides, useful in molecular biology, e.g. in immunoassays or in tracking protein movement in cells.

XX Disclosure; SEQ ID NO 5; 166pp; English.

XX The invention relates to a polynucleotide sequence encoding a Discosoma red fluorescent protein (DsRed) variant having a reduced propensity to oligomerize. The protein variant comprises one or more amino acid substitutions at the AB and/or AC interface(s) of the wild-type DsRed sequence, where the substitutions result in reduced propensity of the DsRed variant to form tetramers and where the variant displays detectable fluorescence of at least one red wavelength. The composition and methods are useful in producing red fluorescent proteins having reduced propensity for oligomerization, especially tetramerization. The protein may be used in molecular biology and in other scientific applications, such as in immunoassays or hybridization assays, or in tracking the movement of proteins in cells. This sequence corresponds to the DsRed coding sequence for the variant T1.

XX Sequence 678 BP; 141 A; 225 C; 205 G; 107 T; 0 U; 0 Other;
 SQ Query Match Score 41.6; DB 11; Length 678;
 Best Local Similarity 53.0%; Pred. No 0.44;
 Matches 89; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
 Qy 2 CCGAGTGGAGGAACATACCGGTGGACAGCTGGACACCTACCTGTGGCACCCC 61
 Db 206 CCAGGTGAGCTGAAAGCCGCCGAAATCCTCGACTACAAGTGTCCCTCCGG 265
 Qy 62 TGGGGGACAAACCCGACTSCATCAAGATCTGGCCAAAGAACGGCGGTCACTAGGGCTACT 121
 Db 265 AGGGTTCAAGTGGAGGGGTGATGAATTCTGGAGGGGGTGACCGTGACCC 325
 Qy 122 GCTACGGTTCAGTGGTGTGGTGTGGAGGACAGAGTCA 169
 Db 326 AGGACTCCCTCCCTGCAAGGGGTCCTCATCPACAAGGTGANGTTCA 373

SQ Sequence 681 BP; 146 A; 223 C; 205 G; 107 T; 0 U; 0 Other;

RESULT 9
 ADC24134 standard; DNA; 681 BP.
 XX AC ADC24134;
 XX DT 18-DEC-2003 (first entry)
 XX DB Discosoma wild-type red fluorescent protein DNA #2.
 XX KW Discosoma red fluorescent protein; DsRed; AB interface; AC interface;
 KW fluorescence energy resonance transfer; FRET; protein kinase;
 KW protein phosphatase; ion indicator; ds.
 XX OS Discosoma.
 PN US2003059835-A1.
 XX PD 27-MAR-2003.
 XX PF 10-APR-2002; 2002US-00121258.
 PR 26-FEB-2001; 2001US-00194308.
 XX (TSIB/) TSIEN R Y.
 PA (CAMP/) CAMPBELL R E.
 PI Tsien RY, Campbell RE;
 XX DR WPI: 2003-743764/70.
 DR P-PSDB; ADC24126.

PT Novel polynucleotide sequence encoding Discosoma red fluorescent protein variant having a reduced propensity to oligomerize, useful for detecting transcriptional activity.

XX Disclosure; SEQ ID NO 9; 67pp; English.

XX The invention describes a polynucleotide sequence (I) encoding a Discosoma red fluorescent protein (DsRed) variant having a reduced propensity to oligomerise, comprising amino acid substitutions at the AB and/or AC interfaces of the wild-type DsRed sequence (S1) comprising 225 amino acids, given in the specification, where the substitutions result in reduced propensity of the DsRed variant to form tetramers. (I) is useful for detecting transcriptional activity by providing a host cell containing a vector which comprises (I) operatively linked to an expression control sequence, and an unit to assay the variant fluorescent protein fluorescence, and assaying fluorescence of the variant fluorescent protein produced by (VII), where variant fluorescent protein fluorescence is indicative of transcriptional activity. A polynucleotide encoding a fusion protein is useful for the analysis of in vivo localisation or trafficking of a polypeptide of interest. A polypeptide marker is useful as markers to identify the location and amount of a target protein produced, where the target protein is fused to the marker, as a complement to or alternative for the green fluorescent protein or its spectral variant, for detecting induction of transcriptions, in applications involving fluorescence energy resonance transfer (FRET), which detects events as the function of the movement of fluorescent donors and acceptors towards or away from each other, for making fluorescent sensors for protein kinase and phosphatase activities or indicators for ions and molecules such as Ca²⁺, Zn²⁺, for identifying the presence of a molecule in a sample, for identifying a specific interaction of a first and second molecule for determining whether a sample contains an enzyme or for determining the pH of the sample. (I) is useful for identifying a region or condition that regulates the activity of an expression control sequence. This sequence represents a modified Discosoma wild-type red fluorescent protein coding region with humanised codon usage.

XX SQ Query Match Score 41.6; DB 10; Length 681;
 Best Local Similarity 53.0%; Pred. No 0.44;
 Matches 89; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
 Qy 2 CCCACGCCAGGAACATACCGGTGGACAGCTGGACACCTACTCTGTGGCACCCC 61
 Db 209 CCAGGTGCTACCTGAAGACCCGCCACATCCCGACTACAAGAAGCTGTCTTCCCG 268
 Qy 62 TGGGGGAAACCCGACTSCATCAAGATCTGGCCAAAGAACGGCGGTCACTAGGGCTACT 121
 Db 269 AGGGTTCAAGTGGAGGGGTGATGAATTCTGGAGGGGGTGACCGTGACCC 328
 Qy 122 GCTACGGTTCAGTGGTGTGGTGTGGAGGACAGTCA 169
 Db 329 AGGACTCCCTGCAAGGGGTCCTCATCPACAAGGTGANGTTCA 376

RESULT 10
 ADL46205 standard; DNA; 681 BP.
 XX ID ADL46205
 AC ADL46205;
 XX DT 20-MAY-2004 (first entry)
 XX DB Human codon optimised Discosoma red fluorescent protein (DsRed) DNA.
 XX DS Human codon optimised Discosoma red fluorescent protein (DsRed) DNA.
 KW DS Gene; red fluorescent protein; DsRed; fluorescence; red wavelength; oligomerization; tetramerization; immunoassay; hybridization assay.
 XX OS Discosoma sp.
 PN WO2003086446-A1.
 XX DR WO2003086446-A1.
 XX PN WO2003086446-A1.

PD 23-OCT-2003.
 XX PR 10-APR-2002; 2002US-00121258.
 PP PR 29-JUL-2002; 2002US-00229208.
 PR XX (REGC) UNIV CALIFORNIA.
 PR XX Tsien RY, Campbell RE, Baird GS,
 PA XX (REGC) UNIV CALIFORNIA.
 PA XX WPI; 2003-845265/78.
 PI Tsien RY, Campbell RE, Baird GS,
 XX DR WPI NO 23; 166pp; English.
 PT New monomeric and dimeric Anthozoan fluorescent protein variants with
 PT reduced propensity to oligomerize, and encoding polynucleotides, useful
 PT in molecular biology, e.g. in immunoassays or in tracking protein
 PT movement in cells.
 XX Disclosure; SEQ ID NO 3; 166pp; English.
 PS The invention relates to a polynucleotide sequence encoding a Discosoma
 CC red fluorescent protein (DsRed) variant having a reduced propensity to
 CC oligomerize. The protein variant comprises one or more amino acid
 CC substitutions at the AB and/or AC interface(s) of the wild type DsRed
 CC sequence, where the substitutions result in reduced propensity of the
 CC DsRed variant to form trimers and where the variant displays detectable
 CC fluorescence of at least one red wavelength. The composition and methods
 CC are useful in producing red fluorescent proteins having reduced
 CC propensity for oligomerization, especially tetramerization. The protein
 CC may be used in molecular biology and in other scientific applications,
 CC such as in immunoassays or hybridization assays, or in tracking the
 CC movement of proteins in cells. This sequence corresponds to the DsRed
 CC coding sequence with codons optimised for human expression.
 XX Sequence 681 BP; 146 A; 223 C; 205 G; 107 T; 0 U; 0 Other;
 SQ Score 41.6%; Score 41.6%; Score 41.6%; Score 41.6%;
 Best Local Similarity 53.0%; Pred. No. 0.44; Length 681;
 Matches 89; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
 Qy 2 CCGACGTGCCAGGGAACTACCGCTGACAGCTCGGACAACACCTTACCTGCGACCCC 61
 Db 209 CCAAGGTGACTGTGAAGCACCCCGACTGCATCAAGATCTGCGAGTCAGCTACT 211
 Qy 62 TGGGGACAAACCCGGACTGCATCAAGATCTGCGAGTCAGCTACTGCGCTACT 121
 Db 269 AGGGCTTCAAGTGGGGCGCTGTGATGAACTTCGAGGACGGCGCTGGTGAACCTGACCC 328
 Qy 62 GCTACCGTTCAAGTGGGGCGCTGTGATGAACTTCGAGGACGGCGCTGGTGAACCTCA 169
 Db 269 AGGGCTTCAAGTGGGGCGCTGTGATGAACTTCGAGGACGGCGCTGGTGAACCTCA 376
 Qy 122 GCTACCGTTCAAGTGGGGCGCTGTGATGAACTTCGAGGACGGCGCTGGTGAACCTCA 169
 Db 329 AGGACTCTCTCCCTGAGGACGGCTGCTCATCTACAGTGAAATTCA 376
 RESULT 12
 AAA48743 ID AAA48743 standard; cDNA; 695 BP.
 XX AC AAA48743;
 ID ADL46225 DT 19-SEP-2000 (first entry)
 XX AC Humanised Discosoma sp. "red" novel fluorescent protein drFP583 CDNA.
 AC ADL46225; DE Humanised Discosoma sp. "red" novel fluorescent protein drFP583 CDNA.
 DT 20-MAY-2004 (first entry)
 XX DE Anthozoan; drFP583; fluorescent protein; non-bioluminescent organism;
 DE fluorescent labeling; ss.
 XX OS Discosoma sp; "red".
 KW OS Synthetic.
 KW ,PN WO200343426-A1.
 XX PD 15-JUN-2000.
 XX PR 10-DEC-1999; 99WO-US029473.
 XX PR 11-DEC-1998; 98US-00210330.

XX OS Discosoma sp.
OS Mammalia.
OS Synthetic.
XX Key CDS
FH Location/Qualifiers
FT 1..723
FT /'tag= a
FT /product= "Mammalian codon optimised Discosoma red
FT fluorescent protein"
FT /transl_except= (pos:616..618,aa:His)
XX WO2002992-A2.
XX PD 28-NOV-2002.
PF 20-MAY-2002; 2002WO-US015968.
XX PR 18-MAY-2001; 2001US-0291871P.
XX PA (RIGE-) RIGEL PHARM INC.
XX PI Peelle B;
XX DR WPI; 2003-120798/11.
DR P-PSDB; ABP56678.
XX New Discosoma red fluorescent protein, useful for functional screens as a
PT reporter for gene transcription, for target characterization and
PT localization of fusion proteins, or for scaffolds for protein and peptide
PT libraries.
XX PS Example 1; Fig 1; 22pp; English.
XX The present invention describes an isolated Discosoma red fluorescent
CC protein (1) comprising a 241 residue amino acid sequence (see ABP56678,
CC S1), with one or more point mutations at amino acid position N24, F125,
CC K164, or M183. Also described: (1) a fusion protein comprising (1); (2)
CC an isolated nucleic acid encoding (1); (3) a vector comprising the
nucleic acid of (2); (4) a host cell comprising the vector; (5) a
CC retroviral cDNA expression library comprising the nucleic acid of (2), or
encoding (1), and (6) methods of making fluorescent variant. The
Discosoma red fluorescent proteins are useful for functional screens as a
CC reporter for gene transcription (e.g. as a fusion protein), for target
characterisation and localisation of fusion proteins, or for scaffolds
for protein and peptide libraries. The fluorescent proteins can also be
used as selectable markers or reporter molecules for a variety of
CC biosassays, including methods that use fluorescence activated cell sorting
(FACS) as a selection mechanism. The method of directed protein evolution
is useful for obtaining improved variants of red fluorescent protein. The
variants of Discosoma red fluorescent protein have greatly improved
CC brightness, expression, and/or folding kinetics as compared to wild type
or a codon optimised variant. The present sequence encodes a mammalian
CC codon optimised Discosoma red fluorescent protein, which is used in an
example from the present invention
XX Sequence 723 BP; 161 A; 233 C; 221 G; 108 T; 0 U; 0 Other;
SQ Score 41.6; DB 8; Length 723;
Query Match 23.5%; Best Local Similarity 53.0%; Pred. No. 0.44%;
Matches 89; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
Qy 2 CGGAGTCCAGGGAACTACCGGCTGGACAGCTCGACACCTACTGTGGCACCCC 61
Db 209 CCAAAGTGATGAGCACTCCGGACTAACAGAAGCTGTCCTTCGG 268
Qy 62 TGGGCCAACCCGAACTGATCAGATGCCAGAGAACGGCTCGACTACGGCTACT 121
Db 269 AGGGCTTCAACTGGGAGCGCTGTGATACCTGGAGACGGCTGGGACCGTGACCC 328
SQ Sequence 1638 BP; 445 A; 450 C; 419 G; 324 T; 0 U; 0 Other;
Query Match 23.5%; Best Local Similarity 53.0%; Pred. No. 0.48%;
Matches 89; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Query Match 23.5%; Best Local Similarity 53.0%; Pred. No. 0.48%; Length 1638;
Matches 89; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

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Db	209	CCAAGGTGTACGTGAAAGCACCCTCCGACATCCCCGACTAACAGAAGCTGTCCCTTCCCG	268
Qy	62	TGGGGACACCCGAACTGATCAAGATTCGCAAGAACGGCTGGCTGCAACTACGGCTACT	121
Db	269	AGGCCTTCAGTGGAAGCCGGTGTGAACTTCGAGAACCTCGAGACCCGGGTGGTGAACCC	328
Qy	122	GCTACGGCGTCCACTGTGTTGTGCAAGTCTGAGGGACAGAACGTCA	169
Db	329	AGGACTCCCTCCCTGAGGAGGGCTCATCTACAAGTGAATTCA	376

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	5	41.6	23.5	316	3 AF491132_32		
	6	41.6	23.5	675	6 AX824731		
	7	41.6	23.5	678	6 AX370404		
	8	41.6	23.5	678	6 AX370406		
	9	41.6	23.5	678	6 AX370408		
	10	41.6	23.5	678	6 AX824725		
	11	41.6	23.5	678	6 AX824732		
	12	41.6	23.5	723	6 AR57331		
	13	41.6	23.5	1050	6 AX66133		
	14	41.6	23.5	2721	6 CQ882115		
	15	41.6	23.5	2772	6 CO882117		
	16	41.6	23.5	4488	6 CQ84509		
	17	41.6	23.5	4692	6 AX463702		
	18	41.6	23.5	6423	12 AY613997		
	19	41.6	23.5	6893	6 AX823860		

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 (without alignments)
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 9: gb_dr: *
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 13: gb_un: *
 14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

RESULT 1
 AF151798 LOCUS Mesobuthus martensii (Buthus martensii) mRNA, complete
 DEFINITION Mesobuthus martensii insect beta-neurotoxin (bt) mRNA, complete
 cds
 AF151798 ACCESSION AF151798.2
 VERSION GI:538289329
 KEYWORDS Mesobuthus martensii (Buthus martensii)
 SOURCE Mesobuthus martensii
 ORGANISM Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 Buthidae; Buthoidea; Buthidae; Mesobuthus.
 REFERENCE 1 (bases 1 to 354)
 AUTHORS Zeng, X.-C., Li, W.-X. and Zu, S.-Y.
 TITLE A novel cDNA sequence encoding the precursor of a new type of insect beta-neurotoxin, BmKBT from Chinese scorpion Buthus martensii Karsch
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 354)
 AUTHORS Li, W.-X., Zeng, X.-C. and Zu, S.-Y.
 TITLE Direct Submission
 JOURNAL Submitted (15-MAY-1999) Department of Virology and Molecular Biology, Wuhan University, Wuhan, Hubei 430072, P.R. China
 REFERENCE 3 (bases 1 to 354)
 AUTHORS Li, W.-X., Zeng, X.-C. and Zu, S.-Y.
 TITLE Direct Submission
 JOURNAL Submitted (05-OCT-2004) Department of Virology and Molecular Biology, Wuhan University, Wuhan, Hubei 430072, P.R. China
 REMARK Sequence update by submitter
 COMMENT On Oct 6, 2004 this sequence version replaced gi:30844240.
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ALIGNMENTS

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		DEFINITION	23/30	Streptomyces avermitilis genomic DNA, complete genome, section	
		ACCESSION	AP005043 BA0000030		
		KEYWORDS	AP005043.1 GI:29609103		
		SOURCE		Streptomyces avermitilis MA-4680	
		ORGANISM		Streptomyces avermitilis MA-4680	
		BACTERIA		Bacterium; Actinobacteria; Actinomycetales; Streptomyces	
		STREPTOMYCETACEAE; Streptomyces.			
1		REFERENCE	1	Omura,S., Ikeda,H., Ishikawa,J., Hanamoto,A., Takahashi,C., Shinose,M., Takahashi,Y., Horikawa,H., Nakazawa,H., Onoae,T., Kikuchi,H., Shiba,T., Sakaki,Y. and Hattori,M.	
		AUTHORS		Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites	
		JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 98 (21), 12215-12220 (2001)		
		MEDLINE	2147403		
		PUBMED	11572948		
REFERENCE 2		AUTHORS	2	Ikeda,H., Ishikawa,J., Hanamoto,A., Shinose,M., Kikuchi,H., Shiba,T., Sakaki,Y. and Hattori,M.	
		JOURNAL	Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis		
		MEDLINE	22608306		
		PUBMED	12692562		
RESULTS		REFERENCE 3	(bases 1 to 299925)	Omura,S., Ikeda,H., Ishikawa,J., Hanamoto,A., Takahashi,C., Shinose,M., Takahashi,Y., Horikawa,H., Nakazawa,H., Onoae,T., Kusuda,N., Director-General of Biotechnology Center, Shiba,T., Sakaki,Y. and Hattori,M.	
AY282464		AUTHORS		Ishikawa(*2), Akiharu Hanamoto(*3), Chigusa Takahashi(*3), Mayumi Shinose(*3), Hiroshi Horikawa(*4), Hidekazu Nakazawa(*4), Tomomi Onoae(*4), Norihiro Kushida(*4), Hisashi Kikuchi(*4), Tadayoshi Shiba(*5), Yoshiyuki Sakai(*6,*7), Maahira Hattori(*1,*7)	
LOCUS		JOURNAL		This work was done in collaboration with Haruo Jun and Satoshi Omura (*1,*3).	
DEFINITION Mesobuthus martensii toxin KBT precursor,		TITLE		Final finishing process and all annotation were done by H. Ikeda and J. Ishikawa.	
VERSION AY282464		KEYWORDS		*1 Kitasato Institute for Life Sciences, Kitasato University	
VERSION AY282464.1		ORGANISM		*2 National Institute of Technology and Evaluation, Biotechnology Center, 2-49-10 Nishihiara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail: bio@nite.go.jp, URL: http://www.bio.nite.go.jp/ , Tel: 81-3-3481-1933, Fax: 81-3-3481-8424)	
REFERENCE 1		REFERENCE		*3 The Kitasato Institute	
AUTHORS Mesobuthus martensii (Butthus martensis)		AUTHORS		*4 National Institute of Technology and Evaluation	
ORGANISM Mesobuthus martensii		JOURNAL		*5 School of Science, Kitasato University	
Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;		TITLE		*6 Institute of Medical Science, University of Tokyo	
Buthida; Buthoidea; Buthidae; Mesobuthus		LOCATION/Qualifiers		*7 RIKEN, Genomic Sciences Center	
REFERENCE 1 (bases 1 to 469)		JOURNAL		Following url is also available.	
AUTHORS Jiang,D., Cao,Z. and Li,W.		TITLE		http://avermilis.kitasono-u.ac.jp.	
JOURNAL Submitted (23-APR-2003) Biotechnology, College of Life Sciences, LuoJia Mountain, Wuhan, Hubei 430072, China		FEATURES			
REFERENCE 1 (bases 1 to 469)		REFERENCE			
AUTHORS Jiang,D., Cao,Z. and Li,W.		AUTHORS			
JOURNAL Submitted (23-APR-2003) Biotechnology, College of Life Sciences, LuoJia Mountain, Wuhan, Hubei 430072, China		JOURNAL			
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Best Local Similarity 53.7%; Pred. No. 3.9;					
Matches 95; Conservative 0; Mismatches 82; Indels 0; Gaps 0;					
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106 . .1536

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complement (1655 . .2782)

/note="SAV544"

/codon_start=1

/transl_table=11

/product="hypothetical protein"

/protein_id="BAC73156_1"

/db_xref="GI: 29609105"

/translation="IMPSPRAPONPSSQSSQASSPSKVKQRDAFFDNAK
YIA1IVFAMGHAWPEPLDHSRAEALMVYTFHMPAFILISGYFSRSFDMDPDRUKR
LTTGCAVAYVLPPEVASYSLSPKRAADNDGHPISILDPPNLTWVALFWRLTTPLNKV
LSTPPVPLAIALAYWAGRMNAAWYHRSOBLGAPWAGTYMTIALEGCSLWVTC
FPFWAPRKMFNTALGACTIYGYLIGFEIAGKSRFENDWYDAMWLQTPYGEVITATVFAA
3488 . .3682

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APSIINRFLDSIAETINSISF"

complement (4060 . .4133)

/gene="tRNA-39"

/product="tRNA-Gly"

/note="codon recognized: GGA

tRNA 39"

/anticodon=(pos:4099 . .4101, aa:Gly)

4287 . .4363

/gene="tRNA-22"

/product="tRNA-Pro"

/note="codon recognized: CCA

tRNA 22"

/anticodon=(pos:4321 . .4323, aa:Pro)

4549 . .5940

/gene="tig"

4549 . .5940

/gene="tig"

/note="SAV546"

/codon_start=1

/transl_table=11

/product="putative cell division trigger factor"

/protein_id="BAC73158_1"

/db_xref="GI: 29609107"

/translation="MKSAVETINPNTVRLTVFEEUDSIDAAYKTKINQOVTVKGF
GAVAVVAAVAVGAYFVIGSGGGSLADDGAHLTTPVLSSEYKRVKGGESSSNSTV"

Query Match 24.7% Score 43.8; DB: 1; Length 299925;

Best Local Similarity 60.5%; Pred. No. 5.5;

Matches 72; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy	48	CCTGTGCGAACCCCTGGGGACACCCGGACTGCAAGATCTGCCAAAGAACGGCGGT	107	DEFINITION Centruroides limpidus limpidus sodium-channel modifier toxin C116 precursor, mRNA, complete cds.
Db	240050	CGTGTGCGGAGAACGGGAGTCGGGGACGGTGCTCCACTCTCCAGAGGTGGCT	240109	ACCESSION AF491132
Qy	108	CGACTACGGCTACTGCTTAAGCGTTCCAGTGTGGTCTGAAGGAGAAGC	166	VERSION GI:31376359
Db	240110	CGACTACGTTCCCTCGCTCCGTTCCGGATTCCGGCCCTGGAGCGGGCGCG	240168	KEYWORD SOURCE
RESULT 4	AP006840_32/c	W COMMENT	Sequence split into 36 fragments LOCUS AP006840 Accession AP006840	ORGANISM Centruroides limpidus limpidus
			Fragment Name	Centruroides limpidus limpidus
			Begin	Centruroides limpidus limpidus
			End	Bukitaya; Metabida; Arthropoda; Chelicera; Arachnida; Scorpiones; Butihida; Butihidae; Butihidae; Centruroides.
				REFERENCE 1 (bases 1 to 316)
				AUTHORS Corona, M. and Possani, L.D.
				TITLE Genes and peptides from the scorpion Centruroides limpidus, that recognize Na(+)-channels
				JOURNAL Unpublished
				REVIEWER 2 (bases 1 to 316)
				AUTHORS Corona, M. and Possani, L.D.
				JOURNAL Direct Submission
				SUBMITTED (12-MAR-2002) Bioestructura Y Reconocimiento Molecular
				JOURNAL Instituto de Biotecnologia, Av. Universidad 2001, Cuernavaca, Morelos 62210, Mexico
				FEATURES Location/Qualifiers
				1. .316 /organism="Centruroides limpidus limpidus"
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				5. . /db_xref="GI:31376360"
				6. . /note="proprotein"
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				12. . /note="encodes proprotein"
				13. . /db_xref="GI:29941"
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				26. . Length
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				28. . Pred. No.
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				32. . Gaps
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ORIGIN		TITLE Patent: WO 0196373-A 3 20-DEC-2001; Clontech Laboratories Inc. (US)
FEATURES	Source	Fluorescent timer proteins and methods for their use
LOCATION/QUALIFIERS		
1.	678	
/organism="synthetic construct"		
/mol_type="unassigned DNA"		
/db_xref="taxon:32630"		
/note="variant of sequence from Discosoma sp."		
ORIGIN		
Query Match	Score 41.6; DB 6; Length 678;	
Best Local Similarity 53.0%; Pred. No. 32;		
Matches 89; Conservative 0; Mismatches 79; Indels 0; Gaps 0;		
Qy 2 CCGACGTGCCAGGGAACTTCCGGTGGACAGCTGGACAAACCTTACTGCGCACCCC 61		
Db 206 CCAAGGTGTAAGTGTGAAAGCACCCTGGACATCCCCGACTACAAGAAGCTGTCCTCCCG 265		
Db 62 TGGGCACAAACGGAACTTCCGGTGGACAGCTGGACAAAGCAGCTGGACTACGGCTACT 121		
Db 266 AGGGCTTCAGTGGGGCTGGGTGATGAACTTGAGGCGGCTGGGACCGTGACCC 325		
Qy 122 GCTAACCGTTTCAAGTGTGGCGACTTCTCTGAAGGAGGAAAGCTCA 169		
Db 326 AGGACTCTCCCTGAGGCGCTGTTACATCTACAGGTGAAGTCA 373		
RESULT 7		
AX370404 LOCUS AX370404 Sequence 1 from Patent WO196373.	678 bp, DNA linear	PAT 16-FEB-2002
ACCESSION AX370404 VERSION AX370404.1	GI:18857490	
KEYWORDS synthetic construct		
SOURCE synthetic construct		
ORGANISM other sequences; artificial sequences.		
REFERENCE 1. Fradkov, A.F. and Teriskikh, A.		
AUTHORS Fluorescent timer proteins and methods for their use		
JOURNAL Patent: WO 0196373-A 1 20-DEC-2001; Clontech Laboratories Inc. (US)		
FEATURES Location/Qualifiers		
1.	678	
/organism="synthetic construct"		
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/db_xref="taxon:32630"		
/note="variant of sequence from Discosoma sp."		
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Query Match	Score 41.6; DB 6; Length 678;	
Best Local Similarity 53.0%; Pred. No. 32;		
Matches 89; Conservative 0; Mismatches 79; Indels 0; Gaps 0;		
Qy 2 CCGACGTGCCAGGGAACTTCCGGTGGACAGCTGGACAAACCTTACTGCGCACCCC 61		
Db 206 CCAAGGTGTAAGTGTGAAAGCACCCTGGACATCCCCGACTACAAGAAGCTGTCCTCCCG 265		
Db 62 TGGGCACAAACGGAACTTCCGGTGGACAGCTGGACAAAGCAGCTGGACTACGGCTACT 121		
Db 266 AGGGCTTCAGTGGGGCTGGGTGATGAACTTGAGGCGGCTGGGACCGTGACCC 325		
Qy 122 GCTAACCGTTTCAAGTGTGGCGACTTCTCTGAAGGAGGAAAGCTCA 169		
Db 326 AGGACTCTCCCTGAGGCGCTGTTACATCTACAGGTGAAGTCA 373		
RESULT 8		
AX370406 LOCUS AX370406 Sequence 3 from Patent WO196373.	678 bp, DNA linear	PAT 16-FEB-2002
ACCESSION AX370406 VERSION AX370406.1	GI:18857491	
KEYWORDS synthetic construct		
SOURCE synthetic construct		
ORGANISM other sequences; artificial sequences.		
REFERENCE 1. Fradkov, A.F. and Teriskikh, A.		
AUTHORS Fluorescent timer proteins and methods for their use		
JOURNAL Patent: WO 0196373-A 5 20-DEC-2001; Clontech Laboratories Inc. (US)		
FEATURES Location/Qualifiers		
1.	678	
/organism="synthetic construct"		
/mol_type="unassigned DNA"		
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/note="variant of sequence from Discosoma sp."		
ORIGIN		
Query Match	Score 41.6; DB 6; Length 678;	
Best Local Similarity 53.0%; Pred. No. 32;		
Matches 89; Conservative 0; Mismatches 79; Indels 0; Gaps 0;		
Qy 2 CCGACGTGCCAGGGAACTTCCGGTGGACAGCTGGACAAACCTTACTGCGCACCCC 61		
Db 206 CCAAGGTGTAAGTGTGAAAGCACCCTGGACATCCCCGACTACAAGAAGCTGTCCTCCCG 265		
Db 62 TGGGCACAAACGGAACTTCCGGTGGACAGCTGGACAAAGCAGCTGGACTACGGCTACT 121		
Db 266 AGGGCTTCAGTGGGGCTGGGTGATGAACTTGAGGCGGCTGGGACCGTGACCC 325		
Qy 122 GCTAACCGTTTCAAGTGTGGCGACTTCTCTGAAGGAGGAAAGCTCA 169		
Db 326 AGGACTCTCCCTGAGGCGCTGTTACATCTACAGGTGAAGTCA 373		
RESULT 10		
AXB4725 LOCUS AX824725 Sequence 7 from Patent WO02066459.	678 bp, DNA linear	PAT 11-DEC-2003
DEFINITION AX824725		
ACCESSION AX824725		
KEYWORDS synthetic construct		
SOURCE synthetic construct		
ORGANISM other sequences; artificial sequences.		
REFERENCE 1. Fradkov, A.F. and Teriskikh, A.		

VERSION	AX824725.1	RESULT 12
KEYWORDS	Discosoma sp.	
ORGANISM	Discosoma sp.	
REFERENCE	Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia;	
AUTHORS	Coralimorpharia; Discosomatidae; Discosoma.	
JOURNAL	1	
FEATURES	Non aggregating fluorescent proteins and methods for using the same	
FEATURES	Patent: WO 0206459-A 7 08-SEP-2002;	
FEATURES	Location/Qualifiers	
ORIGIN	1 .678 /organism="Discosoma sp." /mol_type="unassigned DNA" /db_xref="taxon:86600"	
Query Match	23.5%; Score 41.6; DB 6; Length 678;	
Best Local Similarity	53.0%; Pred. No. 32;	
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Query	2 CGGACGTGGCAGGAACACTACCCGTGGACACAACCTTACCTGTGCCAACCCCC 61	Query Match
Db	206 CCAGGGTGTAACTGTTAAGGCCGCCCCCGCAATTCCTTCCCG 265	Best Local Similarity 53.0%; Pred. No. 31;
Query	62 TGGCGGACAAACCCGAACTTACCCGGACTCATCAAATGCCAGAAAGCCGGTCACTACAGAGCT 121	Mismatches 0; Mismatches 79; Indels 0; Gaps 0;
Db	266 AGGGCTTCAAGTGTGGAGCCGGTGTGATGAACCTCGAACGGGGTGTGACCTGTGACC 325	REF ID: AR527331
Query	122 GCTACAGCCTTCCAGTCAGTGGTGGAGTCTTGAGGACGAAAGCTCA 169	DEFINITION Sequence 1 from patent US 6723537.
Db	326 AGGACTCCTCCCTCGAGGAGGGCTCTATCTACAAGGTGAACTTCA 373	VERSION AR527331
RESULT 11		VERSION AR527331
LOCUS	AX824732	LOCUS AR527331
DEFINITION	Sequence 14 from Patent WO02068459.	DEFINITION Sequence 7 from Patent WO02060941.
VERSION	AX824732	VERSION AX666133
KEYWORDS	AX824732.1 GI:39750595	VERSION AX666133.1 GI:29290961
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
JOURNAL		
FEATURES	Non aggregating fluorescent proteins and methods for using the same	
FEATURES	Patent: WO 0206459-A 14 06-SEP-2002;	
FEATURES	Location/Qualifiers	
ORIGIN	1 .678 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="non-aggregating mutant"	
Query Match	23.5%; Score 41.6; DB 6; Length 678;	
Best Local Similarity	53.0%; Pred. No. 32;	
Matches	0; Mismatches 79; Indels 0; Gaps 0;	
ORIGIN	89; Conservative	
Query	2 CGGACGTGGCAGGAACACTACCCGTGGACACAACCTTACCTGTGCCAACCCCC 61	Query Match
Db	206 CCAGGGTGTAACTGTTAAGGCCGCCCCGCAATTCCTTCCCG 265	Best Local Similarity 53.0%; Pred. No. 30;
Query	62 TGGCGGACAAACCCGAACTTACCCGGACTCATCAAATGCCAGAAAGCT 121	Mismatches 0; Mismatches 79; Indels 0; Gaps 0;
Db	266 AGGGCTTCAAGTGTGGAGCCGGTGTGATGAACCTCGAACGGGGTGTGACCTGTGACC 325	REF ID: AR527331
RESULT 12		DEFINITION Sequence 1 from patent US 6723537.
LOCUS	AX824732	DEFINITION Sequence 7 from Patent WO02060941.
DEFINITION		VERSION AX666133
VERSION		VERSION AX666133.1 GI:29290961
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
JOURNAL		
FEATURES	Non aggregating fluorescent proteins and methods for using the same	
FEATURES	Patent: WO 0206459-A 14 06-SEP-2002;	
FEATURES	Location/Qualifiers	
ORIGIN	1 .678 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="non-aggregating mutant"	
Query Match	23.5%; Score 41.6; DB 6; Length 678;	
Best Local Similarity	53.0%; Pred. No. 32;	
Matches	0; Mismatches 79; Indels 0; Gaps 0;	
ORIGIN	89; Conservative	
Query	2 CGGACGTGGCAGGAACACTACCCGTGGACACAACCTTACCTGTGCCAACCCCC 61	Query Match
Db	206 CCAGGGTGTAACTGTTAAGGCCGCCCCGCAATTCCTTCCCG 265	Best Local Similarity 53.0%; Pred. No. 30;
Query	62 TGGCGGACAAACCCGAACTTACCCGGACTCATCAAATGCCAGAAAGCT 121	Mismatches 0; Mismatches 79; Indels 0; Gaps 0;
Db	266 AGGGCTTCAAGTGTGGAGCCGGTGTGATGAACCTCGAACGGGGTGTGACCTGTGACC 325	REF ID: AR527331
Query	62 TGGCGGACAAACCCGAACTTACCCGGACTCATCAAATGCCAGAAAGCT 169	DEFINITION Sequence 1 from patent US 6723537.
Db	326 AGGACTCCTCCCTCGAGGAGGGCTCTATCTACAAGGTGAACTTCA 373	DEFINITION Sequence 7 from Patent WO02060941.
RESULT 13		DEFINITION Sequence 7 from Patent WO02060941.
LOCUS	AX666133	DEFINITION Sequence 7 from Patent WO02060941.
DEFINITION		DEFINITION Sequence 7 from Patent WO02060941.
VERSION		DEFINITION Sequence 7 from Patent WO02060941.
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
JOURNAL		
FEATURES	Non aggregating fluorescent proteins and methods for using the same	
FEATURES	Patent: WO 0206459-A 14 06-SEP-2002;	
FEATURES	Location/Qualifiers	
ORIGIN	1 .678 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="non-aggregating mutant"	
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Db	494 CCAGGGTGTAACTGTTAAGGCCGCCCCGCAATTCCTTCCCG 553	Best Local Similarity 53.0%; Pred. No. 30;
Query	62 TGGCGGACAAACCCGAACTTACCCGGACTCATCAAATGCCAGAAAGCT 121	Mismatches 0; Mismatches 79; Indels 0; Gaps 0;
Db	554 AGGACTCCTCCCTCGAGGAGGGCTCTATCTACAAGGTGAACTTCA 373	REF ID: AX666133
Query	122 GCTACGGTTCAGTGTGGAGCCGGTGTGAGACTTCTGAAGGACGAAAGCTCA 169	DEFINITION Sequence 1 from patent US 6723537.
Db	554 AGGACTCCTCCCTCGAGGAGGGCTCTATCTACAAGGTGAACTTCA 373	DEFINITION Sequence 7 from Patent WO02060941.

Db ||||| AGGACTCTCCCTGGAGGCGTCCTCATCTACAAGGTGAAGTCA 661
 /note="Description de la séquence artificielle : séquence de fusion"

RESULT 14
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 LOCUS Sequence 1 from Patent WO2004033445.
 DEFINITION
 ACCESSION CO882115
 VERSION 1
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Chavancy, G., Couble, P., Durand, B., Grenier, A.M., Horard, B.,
 Julien, E., Mauchamp, B., Nony, P., Prudhomme, J.C. and Rover, C.
 TITLE Nucleic acid controlling the expression of a useful polypeptide in
 the posterior silk glands of a lepidoptera and application thereof
 Patent: WO 2004033445-A 1 30-SEP-2004;
 Centre National De La Recherche Scientifique-CNRS (FR); UNIVERSITE CLAUDE BERNARD - LYON 1 (FR); Institut National de la Recherche Agronomique (INRA) (FR)
 FEATURES Source
 Location/Qualifiers 1 .2721
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:12630"
 /note="Description de la séquence artificielle : séquence de fusion"

ORIGIN Query Match 23 5%; Score 41 6; DB 6; Length 2721;
 Best Local Similarity 53.0%; Pred. No. 27; Indels 0; Gaps 0;
 Matches 89; Conservative 0; Mismatches 79; Gaps 0;

Qy 2 CGAAGTGGAGGGAACTACCGCTGGACAGGCGACACCTACCGTGCACCC 61
 Db 2249 CCAAGGTGTAAGTGAGCACCCCGCGACATCCCAGACTAACAGCTGTCCTCCCG 2308
 Qy 62 TGGGGACACCCGGACTCATCAAATGCTGCGACTCGACTACCGCTACT 121
 Db 2309 AGGGCTTCAGTGGAGCGCTGATGAACTCGGACGCCGTTGACCTGACCC 2368
 Qy 122 GCTAGCGTCCAGTGTGGTGGAGCTGCTGAAAGGAGAAACTCA 169
 Db 2420 AGGACTCCCTCCCTGGAGGCGCTGCTCATCTACAAGTGAAGTCA 2467

Search completed: July 30, 2005, 19:11:14
 Job time : 1269.87 secs

RESULT 15
 CO882117 2721 bp DNA linear PAT 11-OCT-2004
 LOCUS Sequence 3 from Patent WO2004033445.
 DEFINITION
 ACCESSION CO882117
 VERSION 1
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Chavancy, G., Couble, P., Durand, B., Grenier, A.M., Horard, B.,
 Julien, E., Mauchamp, B., Nony, P., Prudhomme, J.C. and Rover, C.
 TITLE Nucleic acid controlling the expression of a useful polypeptide in
 the posterior silk glands of a lepidoptera and application thereof
 Patent: WO 2004033445-A 3 30-SEP-2004;
 Centre National De La Recherche Scientifique-CNRS (FR); UNIVERSITE CLAUDE BERNARD - LYON 1 (FR); Institut National de la Recherche Agronomique (INRA) (FR)
 FEATURES Source
 Location/Qualifiers 1 .2722
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:12630"

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GenCore version 5.1.6
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4 nucleic - nucleic search, using sw model

on on: July 30, 2005, 18:20:14 : Search time 389.677 Seconds
(without alignments)
2973.108 Million cell updates/sec

Title: US-10-617-978-14.COPY_62_240

Perfect score: 179
Sequence: 1 cggctgacgtccggaaac.....atgagaacgttggaggctctga 179

Scoring table: IDBNNTY_NUC

Gapop 10_0 , Gapext 1_0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Maximum DB seq length: 0
Maximum DB seq 1 length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

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Legend: * = perfect match

Description

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2	38	21..2	316	21 US-10-721-793-141
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4	36..8	20..6	195	21 US-10-721-793-163
5	36..8	20..6	195	21 US-10-721-793-153
6	36..8	20..6	195	21 US-10-721-793-137
7	36..8	20..6	195	21 US-10-721-793-137
8	36..8	20..6	198	21 US-10-721-793-141
9	36..8	20..6	198	21 US-10-721-793-141
10	36..8	20..6	198	21 US-10-721-793-141
11	36..8	20..6	319	21 US-10-721-793-141
12	36..8	20..6	323	21 US-10-721-793-141
13	36..8	20..6	323	21 US-10-721-793-141
14	36..8	20..6	323	21 US-10-721-793-145
15	36..8	20..6	323	21 US-10-721-793-157
16	36..8	20..6	323	21 US-10-721-793-161
17	36..8	20..6	323	21 US-10-721-793-165
18	36..8	20..6	323	21 US-10-721-793-169
19	36..8	20..6	323	21 US-10-721-793-173
20	36..4	20..3	273	21 US-10-721-793-175
21	35..2	19..7	198	21 US-10-721-793-175
22	35..2	19..7	323	21 US-10-721-793-175
23	34..8	19..4	189	21 US-10-721-793-179
24	34..8	19..4	189	21 US-10-721-793-181
25	34..8	19..4	189	21 US-10-721-793-181
26	34..8	19..4	252	21 US-10-721-793-19
27	34..8	19..4	254	21 US-10-721-793-37
28	34..8	19..4	311	21 US-10-721-793-33
29	34..6	19..3	195	21 US-10-721-793-3
30	34..6	19..3	195	21 US-10-721-793-7
31	34..6	19..3	195	21 US-10-721-793-27
32	34..6	19..3	195	21 US-10-721-793-35
33	34..6	19..3	195	21 US-10-721-793-37
34	34..6	19..3	261	21 US-10-721-793-33
35	34..6	19..3	299	21 US-10-721-793-1
36	34..6	19..3	317	21 US-10-721-793-5
37	33..6	18..6	195	21 US-10-721-793-23
38	33..6	18..6	195	21 US-10-721-793-31
39	33..6	18..6	204	21 US-10-721-793-25
40	33..6	18..6	261	21 US-10-721-793-17
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42	33..6	18..6	314	21 US-10-721-793-21
43	33..4	18..7	189	21 US-10-721-793-187
44	33..4	18..7	314	21 US-10-721-793-185
45	32..2	18..0	192	21 US-10-721-793-103

ALIGNMENTS

RESULT 1
US-10-721-793-79

; Sequence 79, Application US/10721793
; Publication No. US20050063331A1
; GENERAL INFORMATION:
; APPLICANT: Corona Villegas, Miguel
; APPLICANT: Garcia Rodriguez, Ma Consuelo
; APPLICANT: Valdez Cruz, Norma Adriana
; APPLICANT: Gurrola Briones, Georgina
; APPLICANT: Becerri Lujan, Baltazar
; APPLICANT: Posani Postay, Lourival Domingos
; TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the Genus Centruroides
; TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
; CURRENT APPLICATION NUMBER: US/10/721-793
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 60/430,067
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 294
; FILE REFERENCE: 2099_0070001
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 79
; LENGTH: 189
; TYPE: DNA
; ORGANISM: Centruroides limpidus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(189)
; OTHER INFORMATION: Product= Sodium-channel modifier toxin
US-10-721-793-9

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description
1	38	21..2	189	21 US-10-721-793-79
2	38	21..2	316	21 US-10-721-793-141
3	36..8	20..6	195	21 US-10-721-793-159
4	36..8	20..6	195	21 US-10-721-793-163
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Query Match 21.2%; Score 38; DB 21; Length 189;
 Best Local Similarity 60.8%; Pred. No. 0; Mismatches 40; Indels 0; Gaps 0;
 Matches 62; Conservative 0; Other INFORMATION:

RESULT 3
 US-10-721-793-139
 Sequence 139, Application US/10721793
 Publication No. US2005006531A1
 GENERAL INFORMATION:
 APPLICANT: Corona Villegas, Miguel
 APPLICANT: Garcia Rodriguez, Ma Consuelo
 APPLICANT: Valdez Cruz, Norma Adriana
 APPLICANT: Gurrola Briones, Georgina
 APPLICANT: Beceril Lujan, Baltazar
 APPLICANT: Possani Postay, Lourival Domingos
 TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the Genus Centruroides
 FILE REFERENCE: 2099 . Version 0070001
 CURRENT APPLICATION NUMBER: US/10/721,793
 CURRENT FILING DATE: 2003-11-26
 PRIOR APPLICATION NUMBER: US 60/430,067
 PRIOR FILING DATE: 2002-12-02
 NUMBER OF SEQ ID NOS: 294
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 139
 LENGTH: 195
 TYPE: DNA
 ORGANISM: Centruroides sculpturatus
 FEATURE: Name/KEY: CDS
 NAME/KEY: CDS
 LOCATION: (1)..(195)
 OTHER INFORMATION: Product= Sodium-channel modifier toxin
 PUBLICATION INFORMATION:
 AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D.
 TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
 TITLE: that recognize Na+-channels
 JOURNAL: Toxicon
 VOLUME: 39
 ISSUE: 12
 PAGES: 1893-1898
 DATE: 2001-12-01
 DATABASE ENTRY DATE:
 RELEVANT RESIDUES: (1)..(195)
 US-10-721-793-139

Query Match 20.6%; Score 36.8; DB 21; Length 195;
 Best Local Similarity 73.4%; Pred. No. 0; Mismatches 17; Indels 0; Gaps 0;
 Matches 47; Conservative 0; Other INFORMATION:

QY 97 AGAACAGGGTGTGATTACGGGTATGCCATTGCTAGCGTTCAAATGGTTGGAATTCTGCA 156
 Db 95 AGAACAGGGTGTGATTACGGGTATGCCATTGCTAGCGTTCAAATGGTTGCGAAGGGTTGC 154

QY 157 AGGA 160
 Db 155 CCGA 158

RESULT 4
 US-10-721-793-143
 Sequence 143, Application US/10721793
 Publication No. US2005006531A1
 GENERAL INFORMATION:
 APPLICANT: Corona Villegas, Miguel
 APPLICANT: Garcia Rodriguez, Ma Consuelo
 APPLICANT: Valdez Cruz, Norma Adriana
 APPLICANT: Gurrola Briones, Georgina
 APPLICANT: Beceril Lujan, Baltazar
 APPLICANT: Possani Postay, Lourival Domingos
 TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the Genus Centruroides
 FILE REFERENCE: 2099 . Version 0070001
 CURRENT APPLICATION NUMBER: US/10/721,793
 CURRENT FILING DATE: 2003-11-26
 PRIOR APPLICATION NUMBER: US 60/430,067
 PRIOR FILING DATE: 2002-12-02

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 Best Local Similarity 60.8%; Pred. No. 0.004; Mismatches 40; Indels 0; Gaps 0;
 Matches 62; Conservative 0; Other INFORMATION:

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 Db 101 TACATTGCTGAAATTGGAGAGAACAAATCTGATGATGATGAGATAGGA 160

QY 108 GTGGATTACGGTATTGCAACGCCCTCCATTAAGATCTGAGAACACCGT 149
 Db 161 GCTGGTACGGCTATTGCAACGCCCTTGGGTGTATTGGAA 202

NUMBER OF SEQ ID NOS: 294
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 143
 LENGTH: 195
 TYPE: DNA
 ORGANISM: Centruroides sculpturatus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1 .. (195)
 OTHER INFORMATION: Product= Sodium-channel modifier toxin
 PUBLICATION INFORMATION:
 AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D.
 TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
 JOURNAL: Toxicon
 VOLUME: 39
 ISSUE: 12
 PAGES: 1893-1898
 DATE: 2001-12-01
 DATABASE ENTRY DATE: (1 .. (195)
 RELEVANT RESIDUES: US-10-721-793-143

Query Match 20.6%; Score 36.8; DB 21; Length 195;
 Best Local Similarity 73.4%; Pred. No. 0.0091;
 Matches 47; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 97 AGAACACGGTGTGGATTACGGTTCAATGCCATTAGCTGGAATTCTCGA 156
 Db 95 AGAACCAAGGAGTAGTTACGGTTCAATGCCATTAGCTGGAATTCTCGA 154

RESULT 6
 US-10-721-793-167
 Sequence 167, Application US/10721793
 Publication No. US20050065331A1
 GENERAL INFORMATION:
 APPLICANT: Corona Villegas, Miguel
 APPLICANT: Garcia Rodriguez, Ma Consuelo
 APPLICANT: Valdez Cruz, Norma Adriana
 APPLICANT: Gurrola Briones, Georgina
 APPLICANT: Becerril Lujan, Baltazar
 APPLICANT: Possani Postay, Lourival Domingos
 TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
 TITLE INVENTION: Venom of Scorpions of the Genus Centruroides
 CURRENT APPLICATION NUMBER: US/10/721,793
 CURRENT FILING DATE: 2003-11-26
 PRIORITY NUMBER: US 60/430,067
 PRIOR FILING DATE: 2002-12-02
 NUMBER OF SEQ ID NOS: 294
 SEQ ID NO: 167
 SOFTWARE: PatentIn version 3.1
 TYPE: DNA
 ORGANISM: Centruroides sculpturatus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1 .. (195)
 OTHER INFORMATION: Product= Sodium-channel modifier toxin
 AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D.
 TITLE: Genes and Peptides from the scorpion Centruroides sculpturatus Ewing,
 TITLE: that recognize Na+-channels
 JOURNAL: Toxicon
 VOLUME: 39
 ISSUE: 12
 PAGES: 1893-1898
 DATE: 2001-12-01
 DATABASE ENTRY DATE: (1 .. (195)
 US-10-721-793-167

Query Match 20.6%; Score 36.8; DB 21; Length 195;
 Best Local Similarity 73.4%; Pred. No. 0.0091;
 Matches 47; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 97 AGAACACGGTGTGGATTACGGTTCAATGCCATTAGCTGGAATTCTCGA 156
 Db 95 AGAACCAAGGAGTAGTTACGGTTCAATGCCATTAGCTGGAATTCTCGA 154

RESULT 7
 US-10-721-793-171

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Sequence 171, Application US/10721793
| Publication No. US2005065331A1
| GENERAL INFORMATION:
| | APPLICANT: Corona Villegas, Miguel
| | APPLICANT: Garcia Rodriguez, Ma Consuelo
| | APPLICANT: Valdez Cruz, Norma Adriana
| | APPLICANT: Gurrola Briones, Georgina
| | APPLICANT: Becerril Lujan, Baltazar
| | APPLICANT: Possani Postay, Lourival Domingos
| TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
| FILE REFERENCE: 2099-0070001
| CURRENT APPLICATION NUMBER: US/10/721,793
| CURRENT FILING DATE: 2003-11-26
| PRIOR APPLICATION NUMBER: US 60/430,067
| PRIORITY FILING DATE: 2002-12-02
| NUMBER OF SEQ ID NOS: 294
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO: 171
| LENGTH: 195
| TYPE: DNA
| ORGANISM: Centruroides sculpturatus
| FEATURE:
| NAME/KEY: CDS
| LOCATION: (1) ..(195)
| OTHER INFORMATION: Product= Sodium-channel modifier toxin
| PUBLICATION INFORMATION:
| AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D.
| TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
| TITLE: that recognize Na+-channels
| JOURNAL: Toxicon
| VOLUME: 39
| ISSUE: 12
| PAGES: 1893-1898
| DATE: 2001-12-01
| DATABASE ENTRY DATE:
| RELEVANT RESIDUES: (1) ..(198)
| US-10-721-793-155

Query Match Score 20.6%; DB 21; Length 198;
Best Local Similarity 73.4%; Pred. No. 0.0092;
Matches 47; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
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Db 95 AGAACACGGTGTGGATTACGGGTTATGCTAGCCCTCAATGCTGGTGAATTTCCTGA 154
RESULT 9
US-10-721-793-159
| Sequence 159, Application US/10721793
| Publication No. US2005065331A1
| GENERAL INFORMATION:
| | APPLICANT: Garcia Villegas, Miguel
| | APPLICANT: Garcia Rodriguez, Ma Consuelo
| | APPLICANT: Valdez Cruz, Norma Adriana
| | APPLICANT: Gurrola Briones, Georgina
| | APPLICANT: Becerril Lujan, Baltazar
| | APPLICANT: Possani Postay, Lourival Domingos
| TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
| FILE REFERENCE: 2099-0070001
| CURRENT APPLICATION NUMBER: US/10/721,793
| CURRENT FILING DATE: 2003-11-26
| PRIOR APPLICATION NUMBER: US 60/430,067
| NUMBER OF SEQ ID NOS: 294
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO: 159
| LENGTH: 198
| TYPE: DNA
| ORGANISM: Centruroides sculpturatus
| FEATURE:
| NAME/KEY: CDS
| LOCATION: (1) ..(198)
| OTHER INFORMATION: Product= Sodium-channel modifier toxin
| PUBLICATION INFORMATION:
| AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D.
| TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
| TITLE: that recognize Na+-channels
| JOURNAL: Toxicon
| VOLUME: 39
| ISSUE: 12
| PAGES: 1893-1898
| DATE: 2001-12-01
| DATABASE ENTRY DATE:
| RELEVANT RESIDUES: (1) ..(198)
| US-10-721-793-159

Query Match Score 20.6%; DB 21; Length 195;
Best Local Similarity 73.4%; Pred. No. 0.0092;
Matches 47; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Qy 97 AGAACACGGTGTGGATTACGGGTTATGCTAGCCCTCAATGCTGGTGAATTTCCTGA 156
Db 95 AGAACACGGTGTGGATTACGGGTTATGCTAGCCCTCAATGCTGGTGAATTTCCTGA 154
RESULT 8
US-10-721-793-155
| Sequence 155, Application US/10721793
| GENERAL INFORMATION:
| | APPLICANT: Corona Villegas, Miguel
| | APPLICANT: Garcia Rodriguez, Ma Consuelo
| | APPLICANT: Valdez Cruz, Norma Adriana
| | APPLICANT: Gurrola Briones, Georgina
| | APPLICANT: Becerril Lujan, Baltazar
| | APPLICANT: Possani Postay, Lourival Domingos
| TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
| FILE REFERENCE: 2099-0070001
| CURRENT APPLICATION NUMBER: US/10/721,793
| CURRENT FILING DATE: 2003-11-26
| PRIOR APPLICATION NUMBER: US 60/430,067
| PRIORITY FILING DATE: 2002-12-02
| NUMBER OF SEQ ID NOS: 294
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO: 155

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Query Match 20 6%; Score 36.8; DB 21; Length 198;
 Best Local Similarity 73.4%; Pred. No. 0.0092%;
 Matches 47; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 97 AGAAACGGTGTGATTAGGGTATTGCTAACGCCCTCAATGCTGGTTGAATTTCGA 156
 Db 95 AGAACCAAGGAGCTAGTTACGGTATTGCTAACGCCATGCTGGTGCAGGTTTC 154

Qy 157 AGGA 160
 Db 155 CCGA 158

RESULT 10

US-10-721-793-163

Sequence 163 Application US/10721793
 Publication No. US2005006531A1
 GENERAL INFORMATION:
 APPLICANT: Corona Villegas, Miguel
 APPLICANT: Garcia Rodriguez, Ma Consuelo
 APPLICANT: Garcia Rodriguez, Ma Consuelo
 APPLICANT: Gurrola Briones, Georgina
 APPLICANT: Recerril Lujan, Baltazar
 APPLICANT: Possani Postay, Lourival Domingos
 TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the Genus Centruroides
 TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
 FILE REFERENCE: 2099-0070001
 CURRENT APPLICATION NUMBER: US/10/721,793
 CURRENT FILING DATE: 2003-11-26
 PRIOR APPLICATION NUMBER: US 60/430,067
 PRIOR FILING DATE: 2002-12-02
 NUMBER OF SEQ ID NOS: 94
 SEQ ID NO: 163
 LENGTH: 198
 TYPE: DNA
 ORGANISM: Centruroides sculpturatus
 FEATURE: CDS
 NAME/KEY: CDS
 LOCATION: (1)..(261)
 OTHER INFORMATION: Product= Sodium-channel modifier toxin precursor
 OTHER INFORMATION: In the mature peptide, the last 2 basic aminoacids are cut

US-10-721-793-153

Query Match 20 6%; Score 36.8; DB 21; Length 198;
 Best Local Similarity 73.4%; Pred. No. 0.0092%;
 Matches 47; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 97 AGAAACGGTGTGATTAGGGTATTGCTAACGCCCTCAATGCTGGTTGAATTTCGA 156
 Db 95 AGAACCAAGGAGCTAGTTACGGTATTGCTAACGCCATGCTGGTGCAGGTTTC 154

Qy 157 AGGA 160
 Db 155 CCGA 158

RESULT 11

US-10-721-793-153

Sequence 153 Application US/10721793
 Publication No. US2005006531A1
 GENERAL INFORMATION:
 APPLICANT: Corona Villegas, Miguel
 APPLICANT: Garcia Rodriguez, Ma Consuelo
 APPLICANT: Valdez Cruz, Norma Adriana
 APPLICANT: Gurrola Briones, Georgina
 APPLICANT: Recerril Lujan, Baltazar
 APPLICANT: Possani Postay, Lourival Domingos

TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
 TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides

FILE REFERENCE: 209-0070001 ; CURRENT APPLICATION NUMBER: US/10/721,793
 CURRENT FILING DATE: 2003-11-26 ; PRIORITY NUMBER: US 60/430,067
 PRIORITY FILING DATE: 2002-12-02 ; NUMBER OF SEQ ID NOS: 294
 SOFTWARE: PatentIn version 3.1 ; SEQ ID NO: 141
 LENGTH: 323 ; TYPE: DNA
 ORGANISM: Centruroides sculpturatus

FEATURE:
 NAME/KEY: CDS
 LOCATION: (5)..(265)
 OTHER INFORMATION: Product= Sodium-channel modifier toxin precursor
 OTHER INFORMATION: In the mature peptide, the last Cys is amidated, and the last Gly
 OTHER INFORMATION: and the last 2 basic aminoacids are cut

FEATURE:
 NAME/KEY: 3'UTR
 LOCATION: (269)..(323)
 OTHER INFORMATION:

FEATURE:
 NAME/KEY: 5'UTR
 LOCATION: (1)..(4)
 OTHER INFORMATION:

FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: (62)..()
 OTHER INFORMATION: Product= Sodium-channel modifier toxin

FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: (5)..(61)
 OTHER INFORMATION:

FEATURE:
 NAME/KEY: 3'UTR
 LOCATION: (259)..(323)
 OTHER INFORMATION: In the mature peptide, the last Cys is amidated, and the last 2 basic aminoacids are cut

FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: (62)..()
 OTHER INFORMATION: Product= Sodium-channel modifier toxin

FEATURE:
 NAME/KEY: 5'UTR
 LOCATION: (1)..(4)
 OTHER INFORMATION:

OTHER INFORMATION:
 PUBLICATION INFORMATION:
 AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D.
 TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
 TITLE: that recognize Na+-channels
 JOURNAL: Toxicon
 VOLUME: 39
 ISSUE: 12
 PAGES: 1893-1898
 DATE: 2001-12-01
 DATABASE ENTRY DATE:
 RELEVANT RESIDUES: (5)..(265)
 US-10-721-793-137

Query Match Score 36.8; DB 21; Length 323;
 Best Local Similarity 73.4%; Pred. No. 0.011; Indels 0; Gaps 0;
 Matches 47; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 97 AGAACACGGTGTGGATTACGGGATTGGCTTCAATGCTGGTGAATTTCAG 156
 DB 156 AGAACCAAGGGTAGTTACGGTATTGGCTTCCATGCTGGCGAACGTTTC 215

QY 157 AGGA 160
 DB 216 CCGA 219

RESULT 13
 US-10-721-793-141
 Sequence 141, Application US/10721793
 Publication No. US20050065331A1

GENERAL INFORMATION:
 APPLICANT: Corona Villegas, Miguel
 APPLICANT: Garcia Rodriguez, Ma Consuelo
 APPLICANT: Valdez Cruz, Norma Adriana
 APPLICANT: Gurrola Briones, Georgina
 APPLICANT: Besserri Lujan, Baltazar
 APPLICANT: Possani Postay, Lourival Domingos
 APPLICANT: Possani Postay, Lourival Domingos
 APPLICANT: Recombinant Immunogens for the Generation of Antivenoms to the
 TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
 TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides

TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
 FILE REFERENCE: 209-0070001 ; CURRENT APPLICATION NUMBER: US/10/721,793
 CURRENT FILING DATE: 2003-11-26 ; PRIORITY NUMBER: US 60/430,067
 PRIORITY FILING DATE: 2002-12-02 ; NUMBER OF SEQ ID NOS: 294
 SOFTWARE: PatentIn version 3.1 ; SEQ ID NO: 141
 LENGTH: 323 ; TYPE: DNA
 ORGANISM: Centruroides sculpturatus

FEATURE:
 NAME/KEY: CDS
 LOCATION: (5)..(265)
 OTHER INFORMATION: Product= Sodium-channel modifier toxin

FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: (5)..(61)
 OTHER INFORMATION:

FEATURE:
 NAME/KEY: 3'UTR
 LOCATION: (259)..(323)
 OTHER INFORMATION: In the mature peptide, the last Cys is amidated, and the last 2 basic aminoacids are cut

FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: (62)..()
 OTHER INFORMATION:

FEATURE:
 NAME/KEY: 5'UTR
 LOCATION: (1)..(4)
 OTHER INFORMATION:

OTHER INFORMATION:
 PUBLICATION INFORMATION:
 AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D.
 TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
 TITLE: that recognize Na+-channels
 JOURNAL: Toxicon
 VOLUME: 39
 ISSUE: 12
 PAGES: 1893-1898
 DATE: 2001-12-01
 DATABASE ENTRY DATE:
 RELEVANT RESIDUES: (5)..(265)
 US-10-721-793-141

Query Match Score 36.8; DB 21; Length 323;
 Best Local Similarity 73.4%; Pred. No. 0.011; Indels 0; Gaps 0;
 Matches 47; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 97 AGAACACGGTGTGGATTACGGGATTGGCTTCAATGCTGGTGAATTTCAG 156
 DB 156 AGAACCAAGGGTAGTTACGGTATTGGCTTCCATGCTGGCGAACGTTTC 215

QY 157 AGGA 160
 DB 216 CCGA 219

RESULT 14
 US-10-721-793-145
 Sequence 145, Application US/10721793
 Publication No. US20050065331A1

GENERAL INFORMATION:
 APPLICANT: Garcia Rodriguez, Miguel
 APPLICANT: Valdez Cruz, Norma Adriana
 APPLICANT: Gurrola Briones, Georgina
 APPLICANT: Besserri Lujan, Baltazar
 APPLICANT: Possani Postay, Lourival Domingos
 APPLICANT: Possani Postay, Lourival Domingos
 APPLICANT: Recombinant Immunogens for the Generation of Antivenoms to the
 TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
 TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides

FILE REFERENCE: 2099.0070001
 CURRENT APPLICATION NUMBER: US/10/721,793
 CURRENT FILING DATE: 2003-11-26
 PRIORITY NUMBER: US 60/430,067
 PRIOR FILING DATE: 2002-12-02
 NUMBER OF SEQ ID NOS: 294
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 145
 LENGTH: 323
 TYPE: DNA
 ORGANISM: Centruroides sculpturatus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (5) .. (265)
 OTHER INFORMATION: Product= Sodium-channel modifier toxin precursor
 OTHER INFORMATION: In the mature peptide, the last Cys is amidated, and the last Gly
 OTHER INFORMATION: and the last 2 basic aminoacids are cut
 FEATURE:
 NAME/KEY: 3'UTR
 LOCATION: (269) .. (323)
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: (62) .. ()
 OTHER INFORMATION: Product= Sodium-channel modifier toxin
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: (5) .. (61)
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: 5'UTR
 LOCATION: (1) .. (4)
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: (5) .. (61)
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: (62) .. ()
 OTHER INFORMATION: Product= Sodium-channel modifier toxin
 PUBLICATION INFORMATION:
 AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D.
 TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
 JOURNAL: Toxicon
 VOLUME: 39
 ISSUE: 12
 PAGES: 1893-1898
 DATE: 2001-12-01
 DATABASE ENTRY DATE:
 RELEVANT RESIDUES: (5) .. (265)
 US-10-721-793-145

CURRENT APPLICATION NUMBER: US/10/721,793
 CURRENT FILING DATE: 2003-11-26
 PRIORITY NUMBER: US 60/430,067
 PRIOR FILING DATE: 2002-12-02
 NUMBER OF SEQ ID NOS: 294
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 157
 LENGTH: 323
 TYPE: DNA
 ORGANISM: Centruroides sculpturatus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (5) .. (265)
 OTHER INFORMATION: Product= Sodium-channel modifier toxin precursor
 OTHER INFORMATION: In the mature peptide, the last 2 basic aminoacids are cut
 FEATURE:
 NAME/KEY: 3'UTR
 LOCATION: (269) .. (323)
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: 5'UTR
 LOCATION: (1) .. (4)
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: (5) .. (61)
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: (62) .. ()
 OTHER INFORMATION: Product= Sodium-channel modifier toxin
 PUBLICATION INFORMATION:
 AUTHORS: Corona, M., Valdez-Cruz, N.A., Merino, E., Zurita, M. & Possani L.D.
 TITLE: Genes and peptides from the scorpion Centruroides sculpturatus Ewing,
 JOURNAL: Toxicon
 VOLUME: 39
 ISSUE: 12
 PAGES: 1893-1898
 DATE: 2001-12-01
 DATABASE ENTRY DATE:
 RELEVANT RESIDUES: (5) .. (265)
 US-10-721-793-145

Query Match 20.6%; Score 36.8; DB 21; Length 323;
 Best Local Similarity 73.4%; Pred. No. 0.011; 17; Indels 0; Gaps 0;
 Matches 47; Conservative 0; Mismatches 17;

Qy	97 AGAACACGGTGTGATTACGGTATGGCTACGCCCTCCATGCTGGTNGAATTTCGA 156
Db	156 AGAACCAAGGGTAGTTACGGTTACGGTATGGCTACGCTTTCGATGCTGGTGCAGCTTGC 215

Query Match 20.6%; Score 36.8; DB 21; Length 323;
 Best Local Similarity 73.4%; Pred. No. 0.011; 17; Indels 0; Gaps 0;
 Matches 47; Conservative 0; Mismatches 17;

Qy	97 AGAACACGGTGTGATTACGGTATGGCTACGCCCTCCATGCTGGTNGAATTTCGA 156
Db	156 AGAACCAAGGGTAGTTACGGTTACGGTATGGCTACGCTTTCGATGCTGGTGCAGCTTGC 215

Query Match 20.6%; Score 36.8; DB 21; Length 323;
 Best Local Similarity 73.4%; Pred. No. 0.011; 17; Indels 0; Gaps 0;
 Matches 47; Conservative 0; Mismatches 17;

Qy	157 AGGA 160
Db	216 CGGA 219

Search completed: July 30, 2005, 20:32:11
 Job time : 390.677 secs

RESULT 15
 US-10-721-793-157
 Sequence 157, Application US/10/721793
 Publication No. US20050065331A1
 GENERAL INFORMATION:
 APPLICANT: Garcia Villegas, Miguel
 APPLICANT: Garcia Rodriguez, Ma Consuelo
 APPLICANT: Valdez Cruz, Norma Adriana
 APPLICANT: Gurrola Briones, Georgina
 APPLICANT: Becerril Lujan, Balazar
 APPLICANT: Possani Postay, Lourival Domingos
 TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
 TITLE OF INVENTION: Venom of Scorpions of the Genus Centruroides
 FILE REFERENCE: 2099.0070001

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GenCore version 5.1.6										GenCore version 5.1.6										
Copyright (c) 1993 - 2005 CompuGen Ltd.					Copyright (c) 1993 - 2005 CompuGen Ltd.					Copyright (c) 1993 - 2005 CompuGen Ltd.					Copyright (c) 1993 - 2005 CompuGen Ltd.					
nucleic - nucleic search, using sw model					nucleic - nucleic search, using sw model					nucleic - nucleic search, using sw model					nucleic - nucleic search, using sw model					
on: July 30, 2005, 17:12:09 ; Search time 85.4775 Seconds					(without alignments)					(without alignments)					(without alignments)					
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Sequence: 1 cggctgacgtccggaaac.....atggaaacctgaaaggctgtga 179					oring table: IDENTITY NUC					oring table: IDENTITY NUC					oring table: IDENTITY NUC					
GapOp 10.0 , Gapext 1.0					GapOp 10.0 , Gapext 1.0					GapOp 10.0 , Gapext 1.0					GapOp 10.0 , Gapext 1.0					
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Listing first 45 summaries																				
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					1: /cggn_6/podata/1/ina/5A_COMB.seq:*					1: /cggn_6/podata/1/ina/5B_COMB.seq:*					1: /cggn_6/podata/1/ina/5B_COMB.seq:*					
					2: /cggn_6/podata/1/ina/5B_COMB.seq:*					2: /cggn_6/podata/1/ina/6A_COMB.seq:*					2: /cggn_6/podata/1/ina/6A_COMB.seq:*					
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					SUMMARIES					SUMMARIES					SUMMARIES					
%					built No.	Score	Query Match	Length	DB ID	Description					%	built No.	Score	Query Match	Length	
					1	42.2	23.6	270	4 US-09-599-632-34	Sequence 34, App1						1	42.2	23.6	270	4 US-09-599-632-34
					2	40.8	22.8	270	4 US-09-599-632-32	Sequence 32, App1						2	40.8	22.8	270	4 US-09-599-632-32
					3	40.8	22.8	270	4 US-09-599-632-36	Sequence 36, App1						3	40.8	22.8	270	4 US-09-599-632-36
					4	32.38	21.2	270	4 US-09-599-632-30	Sequence 30, App1						4	32.38	21.2	270	4 US-09-599-632-30
					5	32.6	18.2	336	3 US-08-931-858B-97	Sequence 97, App1						5	32.6	18.2	336	3 US-08-931-858B-97
					6	32.6	18.2	336	3 US-08-981-739-97	Sequence 97, App1						6	32.6	18.2	336	3 US-08-981-739-97
					7	32.6	18.2	336	3 US-08-981-739-106	Sequence 106, App1						7	32.6	18.2	336	3 US-08-981-739-106
					8	32.6	18.2	336	3 US-09-128-026-97	Sequence 97, App1						8	32.6	18.2	336	3 US-09-128-026-97
					9	32.6	18.2	336	3 US-09-128-026-106	Sequence 106, App1						9	32.6	18.2	336	3 US-09-128-026-106
					10	32.6	18.2	336	4 US-09-220-616-97	Sequence 97, App1						10	32.6	18.2	336	4 US-09-220-616-97
					11	32.6	18.2	336	4 US-09-220-616-106	Sequence 106, App1						11	32.6	18.2	336	4 US-09-220-616-106
					12	32.6	18.2	336	4 US-09-220-527-97	Sequence 97, App1						12	32.6	18.2	336	4 US-09-220-527-97
					13	32.6	18.2	336	4 US-09-220-527-106	Sequence 106, App1						13	32.6	18.2	336	4 US-09-220-527-106
					14	32.6	18.2	336	4 US-09-220-527-106	Sequence 97, App1						14	32.6	18.2	336	4 US-09-220-527-106
					15	32.6	18.2	391	3 US-08-931-858B-107	Sequence 107, App1						15	32.6	18.2	391	3 US-08-931-858B-107
					16	32.6	18.2	391	3 US-08-981-739-107	Sequence 107, App1						16	32.6	18.2	391	3 US-08-981-739-107
					17	32.6	18.2	391	3 US-09-128-026-107	Sequence 107, App1						17	32.6	18.2	391	3 US-09-128-026-107
					18	32.6	18.2	391	4 US-09-220-616-107	Sequence 107, App1						18	32.6	18.2	391	4 US-09-220-616-107
					19	32.6	18.2	391	4 US-09-220-527-107	Sequence 107, App1						19	32.6	18.2	391	4 US-09-220-527-107
					20	32.6	18.2	391	4 US-09-220-527-107	Sequence 107, App1						20	32.6	18.2	391	4 US-09-220-527-107
					21	30.2	16.9	3379	4 US-09-220-132-12	Sequence 12, App1						21	30.2	16.9	3379	4 US-09-220-132-12
					22	30.2	16.9	3445	4 US-09-976-594-323	Sequence 323, App1						22	30.2	16.9	3445	4 US-09-976-594-323
					23	30.30	16.8	4238	4 US-09-949-16-17157	Sequence 17157, App1						23	30.30	16.8	4238	4 US-09-949-16-17157
					24	29.8	16.6	726	4 US-09-702-705-1344	Sequence 1344, App1						24	29.8	16.6	726	4 US-09-702-705-1344
					25	29.8	16.6	726	4 US-09-736-457-1344	Sequence 1344, App1						25	29.8	16.6	726	4 US-09-736-457-1344
					26	29.8	16.6	726	4 US-09-614-12B-1344	Sequence 1344, App1						26	29.8	16.6	726	4 US-09-614-12B-1344
					27	29.8	16.6	726	4 US-09-671-325-1344	Sequence 1344, App1						27	29.8	16.6	726	4 US-09-671-325-1344
					28	16.6	16.6	726	4 US-09-671-1344	Sequence 1344, App1						28	16.6	16.6	726	4 US-09-671-1344

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; SOFTWARE: Microsoft Office 97
; SEQ ID NO: 32
; LENGTH: 270
; TYPE: DNA
; ORGANISM: Hottentotta judiaca
; -09-599-632-32

Query Match 22.8%; Score 40.8; DB 4; Length 270;
Best Local Similarity 61.1%; Pred. No. 1.9e-05;
Matches 66; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
Qy 70 ATAATCCGGACTGCAATTAAAGATCTGTCAAACACGGTTACCGGTATTGCTACG 129
Db 131 ATCATGATTATTGCGGACATTGTAAGTAAAGTACATGGATAATGGTATGGTGG 190
Qy 130 CCTTCCAAGGCTGGTGTGAATTTCGAAAGATGAGAACCTGAAAGGTCT 177
Db 191 TCACCTCGTGTGGTGTGAATTGAAAGAGACATCAATATT 238

RESULT 3
US-09-599-632-36
; Sequence 36, Application US/09599632
; Patent No. 6768002
; GENERAL INFORMATION:
; APPLICANT: Herman, Rafael
; APPLICANT: Wong, James F.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1375 US NA
; CURRENT APPLICATION NUMBER: US/09/599,632
; CURRENT FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,410
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Office 97
; SEQ ID NO: 36
; LENGTH: 270
; TYPE: DNA
; ORGANISM: Hottentotta judiaca
; -09-599-632-36

Query Match 22.8%; Score 40.8; DB 4; Length 270;
Best Local Similarity 61.1%; Pred. No. 1.9e-05;
Matches 66; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
Qy 70 ATAATCCGGACTGCAATTAAAGATCTGTCAAACACGGTTACCGGTATTGCTACG 129
Db 131 ATCATGATTATTGCGGACATTGTAAGTAAAGTACATGGATAATGGTATGGTGG 190
Qy 130 CCTTCCAAGGCTGGTGTGAATTTCGAAAGATGAGAACCTGAAAGGTCT 177
Db 191 TCACCTCGTGTGGTGTGAATTGAAAGAGACATCAATATT 238

RESULT 4
US-09-599-632-30
; Sequence 30, Application US/09599632
; Patent No. 6768002
; GENERAL INFORMATION:
; APPLICANT: Herman, Rafael
; APPLICANT: Wong, James F.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1375 US NA
; CURRENT APPLICATION NUMBER: US/09/599,632
; PRIOR APPLICATION NUMBER: 60/140,410
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Office 97
; SEQ ID NO: 30
; LENGTH: 270

; TYPE: DNA
; ORGANISM: Hottentotta judiaca
; -09-599-632-30

Query Match 21.2%; Score 38; DB 4; Length 270;
Best Local Similarity 56.0%; Pred. No. 0.00022;
Matches 93; Conservative 0; Mismatches 70; Indels 3; Gaps 1;
Qy 12 CCGGAAACTACCACCTGATTCTTCCCACAAATACCTACCGTGCCTTGAGGAT 71
Db 76 CCAGGAATTACCGATACTGTATTGTAAGTCAAGCTTAAAT 135
Qy 72 AACGGGACTGATTAGATCCTGCTAGAACACGGTTGGATTACGGTATTGCTAGCC 131
Db 136 AAT--TATTGCTGGACATTGAAAGTACATGGATAAAGTACATGGTATTGGCTC 192
Qy 132 TTCAATGCTGGTGTGAATTTCGAAAGATGAGAACCTGAAAGGTCT 177
Db 193 ACCTCGTGTGGTGTGAATTGAAAGAGACATCGATATT 238

RESULT 5
US-09-599-632-97/c
; Sequence 97, Application US/08931858E
; Patent No. 6222022
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, EUGENE M
; APPLICANT: MILBERANDT, JEFFREY D
; APPLICANT: KOTZBAUER, PAUL T
; APPLICANT: LAMPE, PATRICIA A
; APPLICANT: KLEIN, ROBERT
; APPLICANT: DESAUVAGE, FRED
; TITLE OF INVENTION: PERSÉPHIN AND RELATED GROWTH FACTOR
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,858E
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 971486
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-722-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; -09-931-858E-97

Query Match 18.2%; Score 32.6; DB 3; Length 336;
Best Local Similarity 52.6%; Pred. No. 0.03;
Matches 71; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
Qy 25 CACTGATTCTCGACAATACTTACCTGCTGGCCCTTGGAGATAATCCGGACTGCA 84
Db 285 CACCTGAGCCITCAAGGCTGCTCTGCTCTGAGACGGCTGGCC 226

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RESULT 6
US-08-981-739-97/c
; Sequence 97, Application US/08981739
; Patent No. 622449
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
;           MILLBRANDT, JEFFREY D.
;           KOTZBAUER, PAUL T.
;           LAMPE, PATRICIA A.
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.3.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,739
; FILING DATE: 31-Aug-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/03461
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 976163
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-08-981-739-97

Query Match          18.2%: Score 32.6; DB 3; Length 336;
Best Local Similarity 52.6%; Pred. No. 0.03;
Matches 71; Conservative 0; Mismatches 64; Indels 0; Gaps 0
Gaps 0
Qy   25 CACTGATTCTTCGACAAATACCTAACCTGCGCCCTTGGGAATAATCGGGCTGC 84
Db   285 CACCTGACCCCTTCAAGCCTGCTTCGCTTGATTCGAGACCAAGCCTGCCGCC 226
Qy   85 TTAAGATCTGTCAAACACGGTGTGATTACGGCTACCCCTTCCAATGCTGGT 144
Db   225 TTCAAGCACCACGCCAACAGCTGGCTGAGGCTGAGCTGCTGCCAATGCTGGT 166
Qy   145 GTGAATTCTGAAAG 159
Db   165 GGTCACTAGGAGG 151

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RESULT 7
 US-08-981-739-106/c
 Sequence 106, Application US/08981739
 Patent No. 6232449
 GENERAL INFORMATION:
 APPLICANT: JOHNSON JR., EUGENE M.
 MILBRANDT, JEFFREY D.
 KOTZBAUER, PAUL T.
 LAMPE, PATRICIA A.
 TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
 NUMBER OF SEQUENCES: 176
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL & HAERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MISSOURI
 COUNTRY: US
 ZIP: 63105-1817
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patentin Release #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/981,739
 FILING DATE: 31-Aug-1998
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US97/03461
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 976163
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314) 727-5188
 TELEFAX: (314) 727-6092
 INFORMATION FOR SEQ ID NO: 106:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 336 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 106:
 US-08-981-739-106

Query Match 18.2%: Score 32.6; DB 3; Length 336;
 Best Local Similarity 52.6%; Pred. No. 0.03; Indels 0; G
 Matches 71; Conservative 0; Mismatches 64;

Qy	25	CACTRGATTCTTCGCAATACCTACCTGTCGCCCTTTGGAGATAATCCGGAC
Db	285	CACCTGAGCCCTTCAGGGCTGGCTCTGTGATTCAGAGACCCGGCTGGC

Qy 85 TTAAGATCTGTCAAAACCGTGTGATTACGGTATTGCTACGCCCTCCAATGC
 Db 225 TTCAGCCAACACAGGCCAACGTCAGGCTGAGGCTGAGGCCAAATGG
 Qy 145 GTGAATTCTGAAGG 159
 Db 165 GGTCATCAAGGAAGG 151

RESULT 8
 US-09-128-026-97/c
 Sequence 97, Application US/09128026
 Patent No. 6403335
 GENERAL INFORMATION:
 APPLICANT: JOHNSON JR., EUGENE M.
 MILBRANDT, JEFFREY D.
 APPLICANT: KOTZBAUER, PAUL T.

Page 4

APPLICANT: LAMPE, PATRICIA A.
 TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
 NUMBER OF SEQUENCES: 176
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL & HAERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MISSOURI
 COUNTRY: US
 ZIP: 6105-1817
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/128,026
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 976163
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314) 727-5188
 TELEFAX: (314) 727-6092
 INFORMATION FOR SEQ ID NO: 97:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 336 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-128-026-97

	Query Match	Score	Length
Qy	Best Local Similarity 52.6%; Matches 71;	DB 3; Pred. No. 0; 0.03; Mismatches 0;	32.6; DB 3; Length 33
Db	25 CACTGTATTTCGACAAATACCTGTGGCCCTTGGAGATAA 285 CACCTGAGCTTCAGGCTGCCCTGTGTTCTGTTGAGACCA		
Qy	85 TTAAGATCTCTAGAAACACCGTGGAATTACGGTTATTGTACGCCCT		
Db	225 TTCAGCCACAGGCCAACAGTGCGCTGAGAGCTAGGACTCTG		
Qy	145 GTGAAATTCTGAGG 165 GGTCTCATCAAGGAAAGG	159 151	
Db			

RESULT 9
 US-09-128-026-106/C
 Sequence 106, Application US/09128026
 Patent No. 6403315
 GENERAL INFORMATION:
 APPLICANT: JOHNSON JR., EUGENE M.
 APPLICANT: MILBRANDT, JEFFREY D.
 APPLICANT: KOTZBAUER, PAUL T.
 APPLICANT: LAMPE, PATRICIA A.
 TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
 NUMBER OF SEQUENCES: 176
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL & HAERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MISSOURI
 COUNTRY: US
 ZIP: 63105-1817
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/128,026
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 976163
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314) 727-5188
 TELEFAX: (314) 727-6092
 INFORMATION FOR SEQ ID NO: 106:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 336 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-128-026-106

	Query Match	Score	DB	3;
	Best Local Similarity	18.2%	No.	0 .03 ;
	Matches 71; Conservative	52.6%	Pred.	No. 0 .03 ;
	Mismatches	0	Mismatches	64 ;
Qy	25 CACTTGATTCTTCGGCAATACTAACCTGCGGCCCTT			
Db	285 CACCTGAGCCCTTCAAAGGTGCCTCTGCTGTTGATTC			
Qy	85 TTAAGATTTGTGAAACACGGTGTGGATTACGGTTATGG			
Db	225 TTCAAGCCACCAAGCCTGCAAGCTGCAGCTGAGCTGAGG			
Qy	145 GTGAATTTCCTGAAGG 159			
Db	165 GGTCAATCAGGAGG 151			

RESULT 10
 US-09-1220-616-97/c
 Sequence 97, Application US/09220616
 Patent No. 645937

GENERAL INFORMATION:
 APPLICANT: JOHNSON JR., EUGENE M.
 APPLICANT: MILLBRANDT, JEFFREY D.
 APPLICANT: KOTZBAUER, PAUL T.
 APPLICANT: LAMPE, PATRICIA A.
 TITLE OF INVENTION: PERSPHIN AND RELATED GROWTH
 NUMBER OF SEQUENCES: 176
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL & HAERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MISSOURI
 COUNTRY: US
 ZIP: 63105-1817

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/220,616
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/981,739
 FILING DATE: 31-AUG-1998
 APPLICATION NUMBER: PCT/US97/03461
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.

REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 976163
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314) 727-5188
 TELEFAX: (314) 727-6092
 INFORMATION FOR SEQ ID NO: 97:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 336 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-220-616-97

Query Match 18.2%; Score 32.6; DB 4; Length 336;
 Best Local Similarity 52.6%; Pred. No. 0; Gaps 0;
 Matches 71; Conservative 64; Indels 0; Gaps 0;
 /
 Qy 25 CACTGATCTTCCACAAATACCTAACCTTGCGGACTGTGA 84
 Db 285 CACCTGAGCTTCAAGCTGCCTCTGCTGATTCTGAGACCGGGCTGGCC 226
 Qy 85 TTAAGATCTGTCAGAACAGCTGGATTACGGTTGCTAGGCCATGCTGCT 144
 Db 225 TTACACCACACAGCACAGCTGGCTGAGCTGAGACGGCTGGCC 166
 Qy 145 GTGAAATTCTGAAG 159
 Db 165 GGTCTCAAGGAAG 151

RESULT 11
 US-09-220-616-106/C
 Patent No. 6645937 Application US/09220616

GENERAL INFORMATION:

APPLICANT: JOHNSON JR., EUGENE M.
 APPLICANT: MILBRANDT, JEFFREY D.
 APPLICANT: KOTZBAUER, PAUL T.

APPLICANT: LAMPE, PATRICIA A.

TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS

NUMBER OF SEQUENCES: 176

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWELL & HAERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MISSOURI
 COUNTRY: US
 ZIP: 63105-1817

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/220,527
 FILING DATE: 24-Dec-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/981,739

FILING DATE: 31-Aug-1998

APPLICATION NUMBER: PCT/US97/03461

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, DONALD R.

REFERENCE DOCKET NUMBER: 976163

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 727-5188

TELEFAX: (314) 727-6092

INFORMATION FOR SEQ ID NO: 97:

SEQUENCE CHARACTERISTICS:

LENGTH: 336 base pairs

TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-220-616-106

Query Match 18.2%; Score 32.6; DB 4; Length 336;
 Best Local Similarity 52.6%; Pred. No. 0; Gaps 0;
 Matches 71; Conservative 64; Indels 0; Gaps 0;
 /
 Qy 25 CACTGATCTTCCACAAATACCTAACCTTGCGGACTGTGA 84
 Db 285 CACCTGAGCTTCAAGCTGCCTCTGCTGATTCTGAGACGGGCTGGCC 226
 Qy 85 TTAAGATCTGTCAGAACAGCTGGATTACGGTTGCTAGGCCATGCTGCT 144
 Db 225 TTACACCACACAGCACAGCTGGCTGAGCTGAGACGGCTGGCC 166
 Qy 145 GTGAAATTCTGAAG 159
 Db 165 GGTCTCAAGGAAG 151

RESULT 12

Sequence 97, Application US/09220527

Patent No. 6692943

GENERAL INFORMATION:

APPLICANT: JOHNSON JR., EUGENE M.
 MILBRANDT, JEFFREY D.
 KOTZBAUER, PAUL T.
 LAMPE, PATRICIA A.

TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS

NUMBER OF SEQUENCES: 176

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWELL & HAERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MISSOURI
 COUNTRY: US
 ZIP: 63105-1817

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/220,527
 FILING DATE: 24-Dec-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/981,739

FILING DATE: 31-Aug-1998

APPLICATION NUMBER: PCT/US97/03461

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, DONALD R.

REFERENCE DOCKET NUMBER: 976163

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 727-5188

TELEFAX: (314) 727-6092

INFORMATION FOR SEQ ID NO: 97:

SEQUENCE CHARACTERISTICS:

LENGTH: 336 base pairs

Query Match 18.2%; Score 32.6; DB 4; Length 336;
 Sequence 97, Application US/09220527
 Patent No. 6692943
 GENERAL INFORMATION:
 APPLICANT: JOHNSON JR., EUGENE M.
 MILBRANDT, JEFFREY D.
 KOTZBAUER, PAUL T.
 LAMPE, PATRICIA A.
 TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
 NUMBER OF SEQUENCES: 176
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL & HAERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MISSOURI
 COUNTRY: US
 ZIP: 63105-1817
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/220,527
 FILING DATE: 24-Dec-1998
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/981,739
 FILING DATE: 31-Aug-1998
 APPLICATION NUMBER: PCT/US97/03461
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REFERENCE DOCKET NUMBER: 976163
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314) 727-5188
 TELEFAX: (314) 727-6092
 INFORMATION FOR SEQ ID NO: 97:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 336 base pairs

Best Local Similarity 52.6%; Pred. No. 0.03; 0; Mismatches 64; Indels 0; Gaps 0;

Qy 25 CACTGATTTCGACAAATACCTTACCTTGCGCCCTTGCGGATATACCGACTGGATTACGGTATTGTCTGCCTCCATGGCTGT 144
Db 285 CACCTGAGGTTCAAGGTGCCCTTGTTGTGATTGTGAGACCCGGTGCCTC 226

Qy 85 TTAGATCTGTAGAACACGGTGTGATTACGGTATTGTAGCCTTCATGCTGT 144
Db 225 TTGCCCCACAGCACAGCTGGTGAAGCTGGCTGAGAGCTGAGGCACTGGCT 166

Qy 145 GTGATTCTGAGG 159
Db 165 GGTCTCAAGGAGG 151

RESULT 14
US-09-220-407-97/c
Sequence 97, Application US/09220407
; Patent No. 6716600
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, EUGENE M.
; NUMBER OF SEQUENCES: 23 9
; TITLE OF INVENTION: PERSÉPHIN AND RELATED GROWTH FACTOR
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931,858
; FILING DATE: 31-Aug-1998
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,739
; FILING DATE: 24-Dec-1998
; APPLICATION NUMBER: PCT/US97/03461
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; FILING DATE: 31-Aug-1998
; APPLICATION NUMBER: PCT/US97/03461
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQ ID DESCRIPTION: SEQ ID NO: 106:
; US-09-220-407-97

Query Match 18.2%; Score 32.6; DB 4; Length 336;
Best Local Similarity 52.6%; Pred. No. 0.03; 0; Mismatches 64; Indels 0; Gaps 0;

Qy 25 CACTGATTTCGACAAATACCTTACCTTGCGCCCTTGCGGATATACCGACTGGATTACGGTATTGTCTGCCTCCATGGCTGT 144
Db 285 CACCTGAGGTTCAAGGTGCCCTTGTTGTGATTGTGAGACCCGGTGCCTC 226

Query Match 18.2%; Score 32.6; DB 4; Length 336;
Best Local Similarity 52.6%; Pred. No. 0.03; 0; Mismatches 64; Indels 0; Gaps 0;

Qy 25 CACTGATTTCGACAAATACCTTACCTTGCGCCCTTGCGGATATACCGACTGGAA 84
Db 285 CACCTGAGGTTCAAGGTGCCCTTGTTGTGATTGTGAGACCCGGTGCCTC 226

Qy 145 GTGATTCTGAGG 159
Db 165 GGTCTCAAGGAGG 151

RESULT 15
 US 08-931-858E-107/C
 Sequence 107; Application US/08931858E
 Patent No. 6222022

GENERAL INFORMATION:

APPLICANT: JOHNSON, EUGENE M
 MILBRANDT, JEFFREY D
 APPLICANT: KOTZBAUER, PAUL T
 APPLICANT: LAMPE, PATRICIA A
 APPLICANT: KUBIN, ROBERT
 APPLICANT: DESAUVAGE, FRED
 TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
 NUMBER OF SEQUENCES: 239
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL & HAVERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MO
 COUNTRY: USA
 ZIP: 63105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/931,858E
 FILING DATE:
 CLASSIFICATION: 435

ATTORNEY AGENT INFORMATION:

NAME: HOLLAND, DONALD R
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 971486

TELECOMMUNICATION INFORMATION:

TELEPHONE: 314-727-5188
 TELEFAX: 314-727-6092

INFORMATION FOR SEQ ID NO: 107:

SEQUENCE CHARACTERISTICS:

LENGTH: 391 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-931-858E-107

Query Match 18.2%; Score 32.6; DB 3; Length 391;
 Best Local Similarity 52.6%; Pred. No. 0.032; 0; Gaps 0;
 Matches 71; Conservative 0; Mismatches 64; Indels 0;

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Db	277	TTCAGCCCCAACAGCCAAAGCTGGCTGAGAGTGGCAGCTGGCAATGTTG	GTT 218
Qy	145	GTGAATTCTGAAGG 159	
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Search completed: July 30, 2005, 20:19:10
 Job time : 87.475 secs

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Sequence:	1 cggctacgtccggaaac.....atgagaacgttgaaggctctga 179			
Scoring table:	IDENTITY_NUC			
Scoring table:	Gapext 1.0			
Searched:	34239544 seqs, 19032134700 residues			
Total number of hits satisfying chosen parameters:	68479088			
Minimum DB seq length:	0			
Maximum DB seq length:	2000000000			
Post-processing: Minimum Match 0%	Maximum Match 100%			
Listing first 45 summaries				
Database :	EST:*			
	1: gb_est1:*			
	2: gb_est2:*			
	3: gb_htc:*			
	4: gb_est3:*			
	5: gb_est4:*			
	6: gb_est5:*			
	7: gb_est6:*			
	8: gb_gss1:*			
	9: gb_gss2:*			
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES				
Result No.	Score	Query Length	DB ID	Description
C 1	35	19.6	414 2 AW343516	AW343516 fi45a12.x1
C 2	34.6	19.3	728 8 BZ047564	BZ07564 1kh8gc10.
C 3	33.8	18.9	411 6 CB803038	AMGN0C:M
C 4	33.8	18.9	595 8 BZ506790	BZ506790 BONH122TR
C 5	33.8	18.9	857 8 BH535763	BH535763 BOGQ146TP
C 6	33.6	18.8	1033 9 CNS013FB	AL102785 Drosophili
C 7	33.2	18.5	1092 7 CN063005	CN063005 A92_p39_O
C 8	33	18.4	580 8 BH741832	BH741832 gt3803.9
C 9	33	18.4	644 8 BH675875	BH675875 BOMD338TR
C 10	33	18.4	788 8 BH439076	BH439076 BOGM34TR
C 11	33	18.4	835 8 BZ501283	BZ501283 BONL148TR
C 12	32.8	18.3	637 7 C0686621	C0686621 DG11-2199
C 13	32.6	18.2	426 7 CO141963	CO141963 EST816634
C 14	32.6	18.2	454 7 CO143971	CO143971 EST818642
C 15	32.6	18.2	455 7 CO134638	CO134628 ESTB819299
C 16	32.6	18.2	744 9 CL172321	CL172321 104_374_1
C 17	32.2	18.0	609 7 C058497	C0584797 DG2-108T1
C 18	32.2	18.0	784 8 BZ444956	BZ444956 BONJ066TF
C 19	32	17.9	550 2 BE767482	BE767482 RC0-NT012
C 20	32	17.9	1101 9 CNS014SJ	AL104557 Drosophil
C 21	31.8	17.8	484 5 BQ300487	C014628 ESTB819299
C 22	31.8	17.8	543 2 BF771057	BF771057 RC2-NT004
C 23	31.8	17.8	543 2 BF771157	BF771157 RC2-NT004
C 24	31.8	17.8	546 2 BF770481	BF770481 RC2-NT004

ALIGNMENTS

RESULT 1		DEFINITION		COMMENT	
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	DEFINITION	IMAGE:1640574	Similar to SV: MCM2_XENLA_P55861 DNA REPLICATION		
	IMAGE	1640574	Danio rerio cDNA clone		
	LICENSING	3	Similar to SV: MCM2_XENLA_P55861 DNA REPLICATION		
	FACTOR	MCM2			
	AW343516	AW343516			
	ACCESSION	AW343516			
	VERSION	EST			
	KEYWORDS				
	SOURCE	Danio rerio	(zebrafish)		
	ORGANISM	Danio rerio			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopercyidae; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.				
	REFERENCE	1 (bases 1 to 414)			
	AUTHORS	Sugano,S., Kawakami,K., Johnson,S., Li,F., Marra,M., Eddy,S., Gibson,M., Jost,S., Kucaba,T., Martin,J., Pape,D., Stepcie,M., Theising,B., Ritter,E., Bowers,Y., Wylie,T., Waterston,R., and Wilson,R.			
	TITLE	WashU Zebrafish EST Project 1999			
	JOURNAL	Unpublished (1999)			
	COMMENT	Contact: S.L. Johnson			
		Washington University School of Medicine			
		4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA			
		Tel: 314 286 1800			
		Fax: 314 286 1810			
		Email: estewatson@wustl.edu			
		Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA			
		Sequencing by: Washington University Genome Sequencing Center			
		Seq primer: T7 ET from Amersham			
		High quality sequence stop: 163.			
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		/organism="Danio rerio"			
		/mol_type="mRNA"			
		/strain="AB"			
		/db_xref="Taxon:7955"			
		/clone="IMAGE:2640574"			
		/sex="mixed (one male and one female, including unfertilized eggs)"			
		/dev_stage="adult"			
		/lab_host="DH10B (phage resistant)"			
		/clone_lib="Sugano, Kawakami zebrafish DRA"			
		/note="Vector: pMB18s-FL3; Site 1: DraII (CACTTGTCG); Site 2: DraII (CACCATGCT); 1st strand cDNA was primed with an oligo(dT) primer (ATGGGGCCRTTTTTTTTTT); double-stranded cDNA was ligated to a DraII adaptor			

[TGTGGCCTACTGG], digested and cloned into distinct DraII sites of the pME18S-P_L vector [5'. site CACTGTCG, 3' site CACCATGTC]. XbaI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science) and kindly donated by Dr. Koichi Kawakami. Custom primers for sequencing: 5' end primer CTCTCTCTCTAAAAGCTGCG and 3' end primer CGACCTGAGTCGAGCCACA.

ORIGIN

Query Match	19.6%	Score 35;	DB 2;	Length 414;
Best Local Similarity	54.2%	Pred. No. 1.3;		
Matches	71;	Conservative	0;	Mismatches 60;
			Indels 0;	Gaps 0;

Qy 22 ACCCACTTGTATTCTTCGCAATACTTACCTGCGCCCTTGGAGTAATCGGGACT 81
Db 317 AGCACGTGGTTCTGAGCGGTCTCATATAGCGCAACCGTTGGGCCAGGAGCA 258
Qy 82 GCGATTAAGATCTGTAGAAACACCGTGTGGATTACGGTATTGTGTACGGCTTCAATGCT 141
Db 257 CCATCGAGATCGCGAGAAGAACCTGGTGACAGGGTGACAAATCACCATCCACGCC 198
Qy 142 GTGTGAAATT 152
Db 197 TGTCAAGCTTT 187

RESULT 2
B2047564 BZ047564 728 bp DNA linear GSS 09-OCT-2002
LOCUS kh84cl0.b1 B.oleracea002 Brassica oleracea genomic survey sequence.
DEFINITION E2047564 1 GI:23644179
VERSION E2047564 1
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; Rosids; eu dicots; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 728)
AUTHORS Delehaunty K., Fewell G., Fulton L., McCombie W.R., Miner T., Nash, W., Rabinowicz P.D. and Wilson R.K.
TITLE Whole genome shotgun reads from *Brassica oleracea*
JOURNAL Unpublished (2002)
COMMENT Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: 1kh84 row: c column: 1:0
Seq. primer: -21UTPOT forward
Class: shotgun
High quality sequence start: 92
High quality sequence stop: 551.
Location/Qualifiers 1..728
/organism="Brassica oleracea"
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/clone_lib="B.oleracea002"
/not="Vector: pOTW13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea T010000013 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the Genomic shotgun library prepared at Washington University Genome Sequencing Center."

ORIGIN

Query Match 19.3% Score 34.6%; DB 8; Length 728;
Best Local Similarity 55.4%; Pred. No. 2; Mismatches 54; Indels 0; Gaps 0;

Qy 28 TTGATTCCTCGACATACTTACCTGCGCCCTTGGAGATAATCGGACTGCATTA 87
Db 431 TGGCTTTATGAAATATGGTTCTGTCGGGTTCTCCATGATCAGGACGCCGTC 490
Qy 88 AGATCTGTAGAAACACGGTGTGGATTACGGTATTCTACGCCTTCCAATGCTGGCTG 147
Db 491 ACAGCTGTGGCACAGCGATGACAGATAAAAGTCCCCACACGGTTTGGC 550

Qy 148 A 148
Db 551 A 551

RESULT 3
CB803038 CB803038 411 bp mRNA linear EST 16-MAY-2003
LOCUS AMGNNUC:MRBE4-00005-A2-A rat brain E15 (10375) Rattus norvegicus
DEFINITION CDNA clone mrbe4-00005-a2 5', mRNA sequence.
ACCESSION CB803038
VERSION CB803038.1 GI:29917845
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 411)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00005 row: a column: 2.
FEATURES Location/Qualifiers 1..411
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/clone="mrbe4-00005-a2"
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Qy 16 GAACATACCCACTGATTCTCCGACATACTTACCTGCGCCCTTGGAGATAATC 75
Db 97 GACTCTATAAACTGAACTGAGTTCGGCAAAGCCTATTACTTTCCTCCAGETCAATCGGC 156
Qy 76 CGGACTGATTAAAGATCTGTCAAGAACACGGTGTGGATTACGGTATGCTACGCCTTC 135
Db 157 ATAGAGAATTCTGCAAGAACACGGGGAACACCTACGTGTCAGGCCTTCA 216

RESULT 4
B2506790/C BZ506790/C 595 bp DNA linear GSS 16-DEC-2002
LOCUS BONH22TR BO_1.6.2_KB_tot Brassica oleracea genomic clone BONH22,
DEFINITION Genomic survey sequence.
ACCESSION BZ506790
VERSION BZ506790.1 GI:27028164
KEYWORDS GSS.

Qy	17	AACTACCACTACTGATTCTCCGACAATACTACTACCTGGAGATAATCC	76		RESULT 8
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DEFINITION		gt38903.g1 BoBuds01 Brassica oleracea genomic clone gt38b03 5 ,		BH741832	
LOCUS		genomic survey sequence.		gt38903.g1	
ACCESSION				BH741832	
VERSION				BH741832.1	GI:18876445
KEYWORDS				GSS.	
SOURCE				Brassica oleracea	
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				rosids; eurosids II; Brassicales; Brassicaceae; Brassica.	
REFERENCE			1 (bases 1 to 580)		
AUTHORS			Katari,M., O'Shaughnessy,A., Palmer,L., Bahret,A., Baker,J., Ballja,V., Cunnias,D.M., Kattenberger,F., King,L., Kirchoff,K., Kuit,K., Miller,B., Muller,S., Naschitz,L., Preston,R., Santos,L., Shah,R., Zutavern,T., Dedhai,N., Rabinowicz,P.D. and McCombie,W.R.		
COMMENT			Whole Genome Shotgun Reads from Brassica oleracea (2002b)		
JOURNAL			Unpublished (2002)		
CONTACT			Contact: W. Richard McCombie		
			Lita Annenberg Hazen Genome Sequencing Center		
			Cold Spring Harbor Laboratory		
			PO Box 100, Cold Spring Harbor, NY 11724, USA		
			Tel: 516 367 8884		
			Fax: 516 367 8874		
			Email: mcombie@cshl.org		
			Plate: g138 row: b column: 03		
			Seq.Primer: -21UniRev		
			Class: shotgun		
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ORIGIN					
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CONTACT					
DEPARTMENT					
FROM					
AMERICAN MUSEUM OF NATURAL HISTORY					
PUTTA, S., SMITH, J.J., WALKER, J.A., RONDET, M., WEISROCK, D.,					
MONAGHAN, J., SAMUELS, A.K., KUMP, K., KING, D.C., MANES, N.J.,					
HABERMANN, B., TANAKA, E., BRYANT, S.V., GARDINER, D.M., PARICHY, D.M.					
AND VOSS, S.R.					
From biomedicine to natural history research: EST resources for					
amphibian salamanders					
Putta, S., Smith, J.J., Walker, J.A., Rondet, M., Weisrock, D.,					
Monaghan, J., Samuels, A.K., Kump, K., King, D.C., Manes, N.J.,					
Habermann, B., Tanaka, E., Bryant, S.V., Gardiner, D.M., Parichy, D.M.					
and Voss, S.R.					
From biomedicine to natural history research: EST resources for					
amphibian salamanders					
CONTACT: SR Voss					
Department of Biology					
University of Kentucky					
TH Morgan Building, Lexington, KY 40506, USA					
TeI: 859 257 9888					
Fax: 859 257 1717					
Email: svoss@uky.edu					
The EST is quality trimmed at the ends with a 20 base window and					
quality threshold of 15 (phred quality score). Please visit					
http://salamander.uky.edu For any information (trace, quality files					
etc) regarding this EST.					
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Matches			0; Mismatches 73;	Indels 0; Gaps 0;	
Qy			29 TGATTCTCGACAACTACCTTGCCCTTGGAGATAATCGGACTGCACTAA	88	
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CONTACT					
DEPARTMENT					
FROM					
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CONTACT					
DEPARTMENT					
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Matches			0; Mismatches 55;	Indels 0; Gaps 0;	
Qy			28 TTGATTCTCGACAATAACCTTACCTGTGCCCTTGGAGATAATCCGACTGCATTA	87	
Db			499 TIGCTTTATAGAAATAAGATTCTCCCTGATCAGGCGCCCTC 440		
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CONTACT					
DEPARTMENT					
FROM					
AMERICAN MUSEUM OF NATURAL HISTORY					
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CONTACT					
DEPARTMENT					
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http://salamander.uky.edu For any information (trace, quality files					
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DEPARTMENT					
FROM					
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MONAGHAN, J., SAMUELS, A.K., KUMP, K., KING, D.C., MANES, N.J.,					
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quality threshold of 15 (phred quality score). Please visit					
http://salamander.uky.edu For any information (trace, quality files					
etc) regarding this EST.					
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Db			499 TIGCTTTATAGAAATAAGATTCTCCCTGATCAGGCGCCCTC 440		
COMMENT			/clone lib="BoBuds01"		
JOURNAL					
CONTACT					
DEPARTMENT					
FROM					
AMERICAN MUSEUM OF NATURAL HISTORY					
PUTTA, S., SMITH, J.J., WALKER, J.A., RONDET, M., WEISROCK, D.,					
MONAGHAN, J., SAMUELS, A.K., KUMP, K., KING, D.C., MANES, N.J.,					
HABERMANN, B., TANAKA, E., BRYANT, S.V., GARDINER, D.M., PARICHY, D.M.					
AND VOS, S.R.					

KEYWORDS	Brassica oleracea	FEATURES	Seq primer: TR Class: sheared ends.
SOURCE	Brassica oleracea	source	Location/Qualifiers 1. organism="Brassica oleracea" /mol_type="genomic DNA" /strain="T01000DH3" /db_xref="taxon:3712" /clone="BOGM34"
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REFERENCE	1 (bases 1 to 64)		
AUTHORS	Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.		
TITLE	Whole genome shotgun sequencing of Brassica oleracea		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Chris Town		
	9712 Medical Center Drive, Rockville, MD 20850, USA. Fax: 301-838-3523 Email: cdtown@tigr.org		
	DNA is from a doubled haploid provided by Tom Osborn.		
FEATURES	Seq primer: TR Class: sheared ends.		
SOURCE	1. .644 /organism="Brassica oleracea" /mol_type="genomic DNA" /strain="T01000DH3" /db_xref="taxon:3712" /clone="BOGM34" /clone_lib="BO-2.3 KB" /note="Vector: phOS1; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into phOS1 using BstXI linkers"		
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Qy	28 TTGATTCCTCGAGATACTTACCTGGGACTGCTGGAGATAATCGGACTCTGCATTA 87		
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Qy	88' AGATCTGTCAAGAACACGGTGTGATTACCGGTATTGCTACGCCATGGCTGGT 147		
Db	259 ACAGCTGTGCCAACACGGATGTACAAGAACAGATGTTCCACGGGTTGCG 318		
Qy	148 A 148		
Db	319 A 319		
RESULT 11			
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LOCUS	BONLH48		
DEFINITION	BONLH48T BO 1.6-2 KB tot Brassica oleracea genomic clone BONLH48,		
	genomic survey sequence.		
ACCESSION	BZ501283		
VERSION	BZ501283.1		
KEYWORDS	GI:27017912		
SOURCE	GSS.		
ORGANISM	Brassica oleracea		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassicae.		
REFERENCE	1 (bases 1 to 835)		
AUTHORS	Town, C.D., van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.		
TITLE	Whole genome shotgun sequencing of Brassica oleracea		
JOURNAL	Other_GSS: BONLH48TF		
COMMENT	Contact: Chris Town		
	TIGR		
	9712 Medical Center Drive, Rockville, MD 20850, USA.		
	Tel: 301-838-3523		
	Fax: 301-838-0208		
	Email: cdtown@tigr.org		
	DNA is from a doubled haploid provided by Tom Osborn.		
FEATURES	Seq primer: TR Class: sheared ends.		
SOURCE	1. .835 /organism="Brassica oleracea" /mol_type="genomic DNA" /strain="T01000DH3" /db_xref="taxon:3712" /clone="BONLH48"		
ORIGIN			
	Query Match 18.4%; Score 33; DB 8; Length 835; Best Local Similarity 54.5%; Pred. No. 7.3; Matches 66; Conservative 0; Mismatches 55; Indels 0; Gaps 0;		
Qy	301-838-3523		
Fax: 301-838-0208			
Email: cdtown@tigr.org			
DNA is from a doubled haploid provided by Tom Osborn.			

ORGANISM Aspergillus flavus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Aspergillus.
REFERENCE 1 (bases 1 to 454)
AUTHORS Yu.J., Whitelaw,C.A., Nierman,W.C., Bhattacharjee, D., and Cleveland,T.B.
TITLE Aspergillus flavus expressed sequence tags for identification of genes with putative roles in aflatoxin contamination of crops
JOURNAL FEMS Microbiol. Lett. (2004) In press
COMMENT Contact: Yu J Food and Feed Safety Research Unit USDA/ARS, Southern Regional Research Center 1100 Robert E. Lee Boulevard, New Orleans, LA 70124, USA Tel: 504 286 4405 Fax: 504 286 4419 Email: jiuyu@srrc.ars.usda.gov for clone information

ORGANISM Aspergillus flavus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Aspergillus.
REFERENCE 1 (bases 1 to 455)
AUTHORS Yu,J., Whitelaw,C.A., Nierman,W.C., Bhattacharjee, D., and Cleveland,T.B.
TITLE Aspergillus flavus expressed sequence tags for identification of genes with putative roles in aflatoxin contamination of crops
JOURNAL FEMS Microbiol. Lett. (2004) In press
COMMENT Contact: Yu J Food and Feed Safety Research Unit USDA/ARS, Southern Regional Research Center 1100 Robert E. Lee Boulevard, New Orleans, LA 70124, USA Tel: 504 286 4405 Fax: 504 286 4419 Email: jiuyu@srrc.ars.usda.gov for clone information

FEATURES

Source

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/dev_stage="developmental stages from 18 to 96 hours"
/lab_host="E. coli DH10 T1 resistant cells"
/clone_lib="Aspergillus flavus Normalized cDNA Expression Library"
/clone="pBlueScript (SK+) (Stratagene), antibiotic selection marker: Carbenicillin; Site 1: NotI, at the 5 prime end; Site 2: EcoRI, at the 3 prime end. This normalized cDNA expression library was constructed using a mixture of mycelial cells grown under eight different medium conditions and harvested at 5 time points (18, 24, 48, 72, 96 hours). The poly-A sequence was trimmed off before ligating to vector."

FEATURES

source

1. .454
/organism="Aspergillus flavus"
/mol_type="mRNA"
/strain="NRRL 3357"
/clone="NAPAU67"
/db_xref="taxon:5059"
/db_xref="taxon:5059"
/sex="asexual mycelia"
/cell_type="mycelia"
/dev_stage="developmental stages from 18 to 96 hours"
/lab_host="E. coli DH10 T1 resistant cells"
/clone_lib="Aspergillus flavus Normalized cDNA Expression Library"
/clone="pBlueScript (SK+) (Stratagene), antibiotic selection marker: Carbenicillin; Site 1: NotI, at the 5 prime end; Site 2: EcoRI, at the 3 prime end. This normalized cDNA expression library was constructed using a mixture of mycelial cells grown under eight different medium conditions and harvested at 5 time points (18, 24, 48, 72, 96 hours). The poly-A sequence was trimmed off before ligating to vector."

ORIGIN

Query Match 18.2%; Score 32.6; DB 7; Length 455;
Best Local Similarity 52.6%; Pred. No. 8.4;
Matches 71; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy	37	CCGACATATCCTACCGTGCCTCCCTTGCGAGATAATCCGACTGCAATTAAAGATCTGTC	96	Db
Db	25	CGTCACAAAGCCGTGACCCATTATCGTGAAGATGGTCAGATGATGTC	84	Qy
Qy	97	AGAAAACAGGTGTGATTACGGGTATTCGCTCATGCTGGTGAATTCTGA	156	Db
Db	85	GTCCTCGTCGTGAGGAATGGGAAGTGTGATGCCGCGGGCTGAATCTGGAGA	144	Qy
Qy	157	AGGATGAGAACGTTGA	171	Db
Db	145	AGTGTGGGGCTTGA	159	

Search completed: July 30, 2005, 20:16:19
Job time : 1988.96 secs

RESULT 15

CO134628	CO134628	455 bp mRNA linear EST 17-JUN-2004
LOCUS	ESTM829299	Aspergillus flavus Normalized cDNA Expression Library
DEFINITION	Aspergillus flavus cDNA clone NAPAU67 5	end, mRNA sequence.
ACCESSION	CO134628	
VERSION	CO134628.1	
KEYWORDS	EST.	
SOURCE	Aspergillus flavus	
ORGANISM	Aspergillus flavus	

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ALIGNMENTS						
No.	Score	Query Length	Match Length	DB ID	Description	
1	43.8	24.7	2748	15	US-10-156-761-5636	Sequence 5636, Appl
2	43.8	24.7	9025508	15	US-10-156-761-1	Sequence 1, Appl
3	41.6	23.5	192	21	US-10-156-761-75	Sequence 75, Appl
4	41.6	23.5	316	21	US-10-156-761-793-73	Sequence 793-73, Appl
5	41.6	23.5	675	13	US-10-006-922-38	Sequence 38, Appl
6	41.6	23.5	675	13	US-10-006-964-22	Sequence 13, Appl
7	41.6	23.5	678	13	US-10-006-922-36	Sequence 36, Appl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Match 24.7%; Score 43.8; DB 15; Length 2748;
 Best Local Similarity 60.5%; Pred. No. 0.0007%; Indels 0; Gaps 0;
 Matches 72; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 48 CCTCTGGGACCCCTGGGACAACCGGACTGCATCAAGATCTGCCAGAACGAGCAGGGCT 107
 Db 2598 CGTGTGGGGAGACGGGAGCACGGGGACCCGGAGTCGTCCTCCAGAGGTGGCT 2657

Qy 108 CGACTACGGCTACTGCTTAGCGTTCAGTGTGGCGAGTCTCTGAAGGACGAAAG 166
 Db 2658 CGACTACGGCTACTGCTCCGGATTCCGGCCGCTGGAGCGAGCG 2716

RESULT 2
 US-10-156-761-1
 Sequence 1, Application US/10156761
 GENERAL INFORMATION:
 APPLICANT: OMURA, SATOSHI
 APPLICANT: ISHIDA, HARUO
 APPLICANT: ISHIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHIOKI
 APPLICANT: HATTORI, MASAHIRA
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-262
 CURRENT APPLICATION NUMBER: US/10/156,761
 CURRENT FILING DATE: 2002-05-29
 PRIOR APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-08-02
 NUMBER OF SEQ ID NOS: 15109
 SEQ ID NO 1
 LENGTH: 9025608
 TYPE: DNA
 ORGANISM: Streptomyces avermitilis
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (4187715)
 OTHER INFORMATION: a, t, c, g, other or unknown

US-10-156-761-1

Query Match 24.7%; Score 43.8; DB 15; Length 9025608;
 Best Local Similarity 60.5%; Pred. No. 0.0018%; Indels 0; Gaps 0;
 Matches 72; Conservative 47; Indels 0; Gaps 0;

Qy 48 CCTCTGGGACCCCTGGGACAACCGGACTGCATCAAGATCTGCCAGAACGAGCAGGGCT 107
 Db 6840426 CGTGTGGGGAGACGGGGAGCACGGGGACCCGGAGTCGTCCTCCAGAGGTGGCT 6840485

Qy 108 CGACTACGGCTACTGCTTAGCGTTCAGTGTGGCGAGTCTCTGAAGGACGAAAG 166
 Db 6840486 CGACTACGGCTACTGCTCCGGTTCCGGATTCCGGCTGGAGCGGGCGCG 6840544

RESULT 3
 US-10-721-793-75
 Sequence 75, Application US/10721793
 GENERAL INFORMATION:
 APPLICANT: Corona Villegas, Miguel
 APPLICANT: Garcia Rodriguez, Ma Consuelo
 APPLICANT: Valdez Cruz, Norma Adriana
 APPLICANT: Gurrola Briones, Georgina
 APPLICANT: Becerril Lujan, Baltazar
 APPLICANT: Possani Postay, Lourival Domingos
 TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
 Scorpions of the Genus Centruroides
 FILE REFERENCE: 2039-007001
 CURRENT APPLICATION NUMBER: US/10/721,793
 CURRENT FILING DATE: 2003-11-26
 PRIOR APPLICATION NUMBER: US 60/430,067
 NUMBER OF SEQ ID NOS: 294
 SEQ ID NO 73
 LENGTH: 316
 TYPE: DNA
 ORGANISM: Centruroides limpidus limpidus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (5..(259)
 OTHER INFORMATION: Product= Sodium-channel modifier toxin precursor
 OTHER INFORMATION: In the mature peptide, the last Ser is amidated, and the last Gly
 OTHER INFORMATION: and the last basic aminoacid are cut

US-10-721-793-75

Sequence 75, Application US/10721793
 Publication No. US200506331A1
 GENERAL INFORMATION:
 APPLICANT: Corona Villegas, Miguel
 APPLICANT: Garcia Rodriguez, Ma Consuelo
 APPLICANT: Valdez Cruz, Norma Adriana
 APPLICANT: Gurrola Briones, Georgina
 APPLICANT: Becerril Lujan, Baltazar
 APPLICANT: Possani Postay, Lourival Domingos
 TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
 Scorpions of the Genus Centruroides
 CURRENT APPLICATION NUMBER: US/10/721,793
 CURRENT FILING DATE: 2003-11-26

Query Match 23.5%; Score 41.6; DB 21; Length 192;
 Best Local Similarity 60.7%; Pred. No. 0.0026%;
 Matches 68; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 35 CGGACAAACACCTTACCTCTGGCAGACCCCTGGGACAACCCGGACTGCATCAAGATCTGCC 94
 Db 29 CGGCGTGRAATAATGGGGCTATGAATGGGGCAACAGGTACTGGCATAGATTCGA 88

Qy 95 AGAGAGACCGGCTGACTACGGCTACTGGCTACGGTTCAGGTTGGCGA 146
 Db 89 AAGGGAGAGGGTAACTAGGGCTATGCTACTGGCTATGCTGGGCTGGTGGCGA 140

US-10-721-793-75

RESULT 4
 US-10-721-793-73
 Sequence 73, Application US/10721793
 Publication No. US200506331A1
 GENERAL INFORMATION:
 APPLICANT: Corona Villegas, Miguel
 APPLICANT: Garcia Rodriguez, Ma Consuelo
 APPLICANT: Valdez Cruz, Norma Adriana
 APPLICANT: Gurrola Briones, Georgina
 APPLICANT: Becerril Lujan, Baltazar
 APPLICANT: Possani Postay, Lourival Domingos
 TITLE OF INVENTION: Recombinant Immunogens for the Generation of Antivenoms to the
 Scorpions of the Genus Centruroides
 FILE REFERENCE: 2039-007001
 CURRENT APPLICATION NUMBER: US/10/721,793
 CURRENT FILING DATE: 2003-11-26
 PRIOR APPLICATION NUMBER: US 60/430,067
 NUMBER OF SEQ ID NOS: 294
 SEQ ID NO 73
 LENGTH: 316
 TYPE: DNA
 ORGANISM: Centruroides limpidus limpidus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1..(316)
 OTHER INFORMATION: Product= Sodium-channel modifier toxin precursor
 OTHER INFORMATION: In the mature peptide, the last Ser is amidated, and the last Gly
 OTHER INFORMATION: and the last basic aminoacid are cut

US-10-721-793-73

US-10-721-793-73

Query Match 23.5%; Score 41.6; DB 21; Length 316;
Best Local Similarity 60.7%; Pred. No. 0.0027;
Matches 68; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 35 CGGAAACACTAACCTGGGGCACCCCTGGGACAACCGGACTGATCAAGATCTGCC 94
Db 90 CGGGTGCAAATACGGTGTCTATGAATTGGTGAACCGTTACTGGTAGAATGCA 149

Qy 95 AGAACCCGGCTGACTGGCTACTGGCTTCCAGTGTGGTCGA 146
Db 150 AAGGGAGCGGAACTACGGTATTGGTATACTGTGGTGAAGTCA 201

RESULT 5
US-10-006-922-38
Sequence 38, Application US/10006922
Publication No. US20020197676A1
GENERAL INFORMATION:
APPLICANT: Lukyanov, Konstantin
APPLICANT: Fradkov, Arcady F.
APPLICANT: Matz, Yuliia A.
APPLICANT: Matz, Mikhail V.
TITLE OF INVENTION: Chromophores/Fluorophores and Methods For Using the Same
FILE REFERENCE: CLON-035CIP
CURRENT APPLICATION NUMBER: US/10/006,922
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/120,330
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: 09/157,898
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/158,144
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/158,477
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/157,556
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/144,338
PRIOR FILING DATE: 1999-11-19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 675
TYPE: DNA
ORGANISM: Discosoma species

US-10-006-922-38

Query Match 23.5%; Score 41.6; DB 13; Length 675;
Best Local Similarity 53.0%; Pred. No. 0.003;
Matches 89; Conservative 79; Mismatches 46; Indels 0; Gaps 0;

Qy 2 CCGAGCTGCAAGGAACTACCGCTGGAAAGCTCGACACCTACTGGTGCACCC 61
Db 206 CCAAGGTGTAAGTGGAGCCCGGACTAACAGGCTGTCGGGACCGTGACCC 265

Qy 62 TGGGGACAAACCCGAACTACCGCTGGAAAGCTCGACACCTACTGGTGCACCC 61
Db 265 AGGGTCAAGTGGAGCCCGGACTAACAGGCTGTCGGGACCGTGACCC 325

Qy 122 GCTAGCGTTCCAGTGTGGCTCTGAGGAGGAACTTGAGGACGGTGAAGTCA 169
Db 326 AGGACTCCCTCCCTGGAGGAGGCTCATCTACAAGTGAAGTCA 373

RESULT 7
US-10-006-922-36
Sequence 36, Application US/10006922
Publication No. US20020197676A1
GENERAL INFORMATION:
APPLICANT: Lukyanov, Sergey A.
APPLICANT: Fradkov, Arcady F.
APPLICANT: Matz, Yuliia A.
APPLICANT: Matz, Mikhail V.
APPLICANT: Terskikh, Alexey
TITLE OF INVENTION: Chromophores/Fluorophores and Methods For Using the Same
FILE REFERENCE: CLON-035CIP
CURRENT APPLICATION NUMBER: US/10/006,922
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/120,330
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: 09/157,898
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/158,144
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/158,477
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/157,556
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 09/144,338
PRIOR FILING DATE: 1999-11-19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 678
TYPE: DNA
ORGANISM: Discosoma species

US-10-081-864-13
Sequence 13, Application US/10081864
Publication No. US20030022287A1
GENERAL INFORMATION:
APPLICANT: Lukyanov, Sergey

RESULT 6
US-10-081-864-13
Sequence 13, Application US/10081864
Publication No. US20030022287A1
GENERAL INFORMATION:
APPLICANT: Lukyanov, Sergey

US-10-006-922-36

Query Match 23.5%; Score 41.6; DB 13; Length 678;
Best Local Similarity 53.0%; Pred. No. 0.003; Indels 0; Gaps 0;
Matches 89; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 2 CCGACGTGCCAGGAAACTAACCCGGTGGAACTAGCTGGACAACACTTGTGGCACCCC 61
Db 206 CCAGAGTGTACGTGAAGCCCCGGACTCCCGACTAAGAAAGTGTCTTCCCG 265

Qy 62 TGGCGGACAACCCGACTCATCAAGATCTGGCAGAACAGCGCTCCACTAGGCTACT 121
Db 266 AGGGTTCAACTGGAGCCGGTGTGAACCTGGAGGGCGCTGGACCGTGACCC 325

Qy 122 GCTACGGTTCAGTGTGGCAGTTCTGAGGAGGAGGAGCTCA 169
Db 326 AGGACTCCCTCGAGGAGCTGTCAATCTAACAGGTGAAGTCA 373

RESULT 8
US-10-081-864-7
Sequence 7 Application US/10081864
Publication No. US2003002287A1
GENERAL INFORMATION:
APPLICANT: Lukyanov, Sergey
APPLICANT: Lukyanov, Konstantin
APPLICANT: Yanushhevich, Yurii
APPLICANT: Savitsky, Arcady
APPLICANT: Fradkov, Alexande

TITLE OF INVENTION: No. US2003002287A1 Aggregating Fluorescent Proteins and Methods for Using the Same

FILE REFERENCE: CLON-067

CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: US/10/081,864
CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION NUMBER: 10/006,922
PRIOR FILING DATE: 2001-12-04
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 7
LENGTH: 678
TYPE: DNA
ORGANISM: Discosoma sp

US-10-081-864-7

Query Match 23.5%; Score 41.6; DB 14; Length 678;
Best Local Similarity 53.0%; Pred. No. 0.003; Indels 0; Gaps 0;
Matches 89; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 2 CCGACGTGCCAGGAAACTAACCCGGTGGAACTAGCTGGACAACACTTGTGGCACCCC 61
Db 206 CCAGAGTGTACGTGAAGCCCCGGACTCCCGACTAAGAAAGTGTCTTCCCG 265

Qy 62 TGGCGGACAACCCGACTCATCAAGATCTGGCAGAACAGCGCTCCACTAGGCTACT 121
Db 266 AGGGTTCAACTGGAGCCGGTGTGAACCTGGAGGGCGCTGGACCGTGACCC 325

Qy 122 GCTACGGTTCAGTGTGGCAGTTCTGAGGAGGAGGAGCTCA 169
Db 326 AGGACTCCCTCGAGGAGCTGTCAATCTAACAGGTGAAGTCA 373

RESULT 10
US-10-121-258-5
Sequence 5 Application US/10121258
Publication No. US20030059835A1
GENERAL INFORMATION:
APPLICANT: Tsien, Roger
APPLICANT: Campbell, Robert
TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT PROTEIN VARIANTS AND METHODS FOR MAKING SAME

FILE REFERENCE: UCO83-ICP2CP1

CURRENT APPLICATION NUMBER: US/10/121,258
CURRENT FILING DATE: 2002-04-10
PRIOR APPLICATION NUMBER: 09/794,308
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/866,538
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 678
TYPE: DNA
ORGANISM: Artificial Sequence

US-10-121-258-5

Query Match 23.5%; Score 41.6; DB 14; Length 678;
Best Local Similarity 53.0%; Pred. No. 0.003; Indels 0; Gaps 0;
Matches 89; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 2 CCGACGTGCCAGGAAACTAACCCGGTGGAACTAGCTGGACAACACTTGTGGCACCCC 61
Db 206 CCAGAGTGTACGTGAAGCCCCGGACTCCCGACTAAGAAAGTGTCTTCCCG 265

Qy 62 TGGCGGACAACCCGACTCATCAAGATCTGGCAGAACAGCGCTCCACTAGGCTACT 121
Db 266 AGGGTTCAACTGGAGCCGGTGTGAACCTGGAGGGCGCTGGACCGTGACCC 325

Qy 122 GCTACGGTTCAGTGTGGCAGTTCTGAGGAGGAGGAGCTCA 169
Db 326 AGGACTCCCTCGAGGAGCTGTCAATCTAACAGGTGAAGTCA 373

RESULT 9
US-10-081-864-14
Sequence 14 Application US/10081864
Publication No. US2003002287A1
GENERAL INFORMATION:
APPLICANT: Lukyanov, Sergey
APPLICANT: Lukyanov, Konstantin
APPLICANT: Yanushhevich, Yurii
APPLICANT: Savitsky, Arcady
APPLICANT: Fradkov, Alexande

Query Match 23.5%; Score 41.6; DB 14; Length 678;
Best Local Similarity 53.0%; Pred. No. 0.003; Indels 0; Gaps 0;
Matches 89; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 2 CCGACGTGCCAGGAAACTAACCCGGTGGACAACACTTGTGGCACCCC 61
Db 206 CCAGAGTGTACGTGAAGCCCCGGACTCCCGACTAAGAAAGTGTCTTCCCG 265

Qy 62 TGGCGGACAACCCGACTCATCAAGATCTGGCAGAACAGCGCTCCACTAGGCTACT 121

Db 266 AGGGCTCAAGTGGAGCGGTGATGAACTTCGAGGACGGGGTGGTGCACCC 325
 Qy 122 GCTAGGCTTCCAGTGGTGGTCTGAAGGACAGAACCTCA 169
 Db 326 AGGACTCTCCCTGCCAGGGCTCCTCATCTACAAGGTGAAGTTCA 373

RESULT 11
 US-10-315-920-1
 Sequence 1, Application US/10315920
 Publication No. US20030175809A1
 GENERAL INFORMATION:
 APPLICANT: Fradkov, Arcady Fedorovich
 APPLICANT: Terskikh, Alexey
 TITLE OF INVENTION: FLUORESCENT TIMER PROTEINS AND METHODS
 FILE REFERENCE: FOR THEIR USE
 CURRENT APPLICATION NUMBER: US/10/315,920
 CURRENT FILING DATE: 2002-12-09
 PRIOR APPLICATION NUMBER: 60/211,607
 PRIOR FILING DATE: 2000-06-14
 PRIOR APPLICATION NUMBER: PCT/US01/19097
 PRIOR FILING DATE: 2001-06-13
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 678
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: variant of sequence from Discosoma sp.
 US-10-315-920-1

Query Match 23.5%; Score 41.6; DB 16; Length 678;
 Best Local Similarity 53.0%; Pred. No. 0.003; Indels 0; Gaps 0;
 Matches 89; Conservative 0; Mismatches 79;

Db 2 CCGACGTGCCAGGGAACTTACCGCTGGACAGCTGGACACCTAACCTACCTGGCACCC 61
 Db 206 CCAAAGCTGTTAGTGAGCAACCCGGCAATCCCGGACTACAAAGAGCTCCPTCCCC 265

Qy 62 TGGGGGACAAACCGGAACTGATCAGATCTGGCAGAGCGGGCTGCAACTACGGTACT 121
 Db 266 AGGGCTTCAAGTGGAGGGCTGTGTAACATTGAGGACGGCCGTGTGACCC 325

Qy 122 GCTAGGCTTCCAGTGGTGTGTTCTGAAGGACAGAACCTCA 169
 Db 326 AGGACTCTCCCTGCCAGGGCTCCTCATCTACAAGGTGAAGTTCA 373

OTHER INFORMATION: variant of sequence from Discosoma sp.

RESULT 12
 US-10-315-920-3
 Sequence 3, Application US/10315920
 Publication No. US20030175809A1
 GENERAL INFORMATION:
 APPLICANT: Fradkov, Arcady Fedorovich
 APPLICANT: Terskikh, Alexey
 TITLE OF INVENTION: FLUORESCENT TIMER PROTEINS AND METHODS
 FILE REFERENCE: FOR THEIR USE
 CURRENT APPLICATION NUMBER: US/10/315,920
 PRIOR APPLICATION NUMBER: 60/211,607
 PRIOR FILING DATE: 2000-06-14
 PRIOR APPLICATION NUMBER: PCT/US01/19097
 PRIOR FILING DATE: 2001-06-13
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 678
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: variant of sequence from Discosoma sp.

RESULT 13
 US-10-315-920-5
 Sequence 5, Application US/10315920
 Publication No. US20030175809A1
 GENERAL INFORMATION:
 APPLICANT: Fradkov, Arcady Fedorovich
 APPLICANT: Terskikh, Alexey
 TITLE OF INVENTION: FLUORESCENT TIMER PROTEINS AND METHODS
 FILE REFERENCE: CLON-077CIP
 CURRENT APPLICATION NUMBER: US/10/315,920
 PRIOR APPLICATION NUMBER: CLON-077CIP
 CURRENT FILING DATE: 2002-12-09
 PRIOR APPLICATION NUMBER: 60/211,607
 PRIOR FILING DATE: 2000-06-14
 PRIOR APPLICATION NUMBER: PCT/US01/19097
 PRIOR FILING DATE: 2001-06-13
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 5
 LENGTH: 678
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: variant of sequence from Discosoma sp.

RESULT 14
 US-10-006-922-35
 Sequence 35, Application US/10006922
 Publication No. US200201976A1
 GENERAL INFORMATION:
 APPLICANT: Lukyanov, Sergey A.
 APPLICANT: Fradkov, Arcady F.
 APPLICANT: Labas, Yuliia A.
 APPLICANT: Matz, Mikhail V.
 APPLICANT: Terskikh, Alexey

TITLE OF INVENTION: No. US20020197676A1 el Chromophores/Fluorophores and Methods for Using the Same
 FILE REFERENCE: CLON-035CIP

CURRENT APPLICATION NUMBER: US/10/006,922

PRIOR FILING DATE: 2001-12-04

PRIOR APPLICATION NUMBER: 09/120,330

PRIOR FILING DATE: 1998-12-11

PRIOR APPLICATION NUMBER: 09/457,898

PRIOR FILING DATE: 1999-12-09

PRIOR APPLICATION NUMBER: 09/458,144

PRIOR FILING DATE: 1999-12-09

PRIOR APPLICATION NUMBER: 09/458,477

PRIOR FILING DATE: 1999-12-09

PRIOR APPLICATION NUMBER: 09/457,556

PRIOR FILING DATE: 1999-12-09

PRIOR APPLICATION NUMBER: 09/444,338

PRIOR FILING DATE: 1999-11-19

NUMBER OF SEQ ID NOS: 46

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 35

LENGTH: 681

TYPE: DNA

US-10-006-922-35

; TYPE: DNA
 ; ORGANISM: Discosoma species
 US-10-006-922-37

Query	2	CCGACGTGCCAGGGAACTACCCGCTGGACAGCTGGACAAACCTACCTGTGGCACCCC	61
Match	209	CCAGGTGTACGTGAAGACCCGGACTCGCATCAAGATCTGGAGAACCGGTGACTAGGTACT	268
Best Local Similarity	23.5%	Score 41.6; DB 13; Length 681;	
Matches	89;	Pred. No. 0.003; Mismatches 79; Indels 0; Gaps 0;	
Query	62	TGGCGACAACCCGGAATCGCATCAAGATCTGGAGAACCGGTGACTAGGTACT	121
Db	269	AGGCCTTAAGTGGAGCCGGTATGACTTCAGAGCTGGCGACCTGGACCC	328
Query	122	GCTACGGTTCCAGTGTGGAGTCTGAAGGAGCAGAACGTCAGGAGCTCA	169
Db	329	AAGACTCCCTCTGCAAGGACGGTGTCTCATCTACAGTGAGTCA	376

Search completed: July 30, 2005, 20:32:31
 Job time : 405.323 secs

Query Match 23.5%; Score 41.6; DB 13; Length 681;
 Best Local Similarity 53.0%; Pred. No. 0.003; Mismatches 79; Indels 0; Gaps 0;
 Matches 89; Conservative 0; Gaps 0;

Query	2	CCGACGTGCCAGGGAACTACCCGCTGGACAGCTGGACAAACCTACCTGTGGCACCCC	61
Db	209	CCAGGTGTACGTGAAGACCCGGACTCGCATCAAGATCTGGAGAACCGGTGACTAGGTACT	268
Query	62	TGGCGACAACCCGGAATCGCATCAAGATCTGGAGAACCGGTGACTAGGTACT	121
Db	269	AGGCCTTAAGTGGAGCCGGTATGACTTCAGAGCTGGCGACCTGGACCC	328
Query	122	GCTACGGTTCCAGTGTGGAGTCTGAAGGAGCAGAACGTCAGGAGCTCA	169
Db	329	AAGACTCCCTCTGCAAGGACGGTGTCTCATCTACAGTGAGTCA	376

RESULT 15
 US-10-006-922-37

; Sequence 37, Application US/10006922

GENERAL INFORMATION:

; APPLICANT: Lukyanov, Sergey A.

; APPLICANT: Fradkov, Arcady F.

; APPLICANT: Labas, Yuliia A.

; APPLICANT: Matz, Mikhail V.

; APPLICANT: Terskikh, Alexey

TITLE OF INVENTION: No. US20020197676A1 el Chromophores/Fluorophores and Methods for Using the Same

FILE REFERENCE: CLON-035CIP

CURRENT APPLICATION NUMBER: US/10/006,922

CURRENT FILING DATE: 2001-12-04

PRIOR APPLICATION NUMBER: 09/120,330

PRIOR FILING DATE: 1998-12-11

PRIOR APPLICATION NUMBER: 09/457,898

PRIOR FILING DATE: 1999-12-09

PRIOR APPLICATION NUMBER: 09/458,144

PRIOR FILING DATE: 1999-12-09

PRIOR APPLICATION NUMBER: 09/458,477

PRIOR FILING DATE: 1999-12-09

PRIOR APPLICATION NUMBER: 09/457,556

PRIOR FILING DATE: 1999-12-09

PRIOR APPLICATION NUMBER: 09/444,338

PRIOR FILING DATE: 1999-11-19

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 37

LENGTH: 681

Copyright	GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.	BF982489 BF982489 BF982489 BF982489 BF982489					
nucleic - nucleic search, using sw model		BF30532 BF30532 BF30532 BF30532 BF30532					
on:	July 30, 2005, 15:50:29 ; Search time 1939.04 Seconds (without alignments)	601892806 601892806 601892806 601892806 601892806					
Scoring table:	IDENTITY NUC Gapext 1.0 , Gapext 1.0	60231983 60231983 60231983 60231983 60231983					
Searched:	34239544 seqs, 19032134700 residues	BF981884 BF981884 BF981884 BF981884 BF981884					
Total number of hits satisfying chosen parameters:	68479088	CF144031 CF144031 CF144031 CF144031 CF144031					
Minimum DB seq length: 0		U1-HF-BP0 AW500041 AW500041 AW500041 AW500041					
Maximum DB seq length: 2000000000		CN78122 CN78122 CN78122 CN78122 CN78122					
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Maximum Match 100%		BP266195 BP266195 BP266195 BP266195 BP266195					
Listing first 45 summaries		CD611367 CD611367 CD611367 CD611367 CD611367					
Database :	EST: * 1: 9b_est1: * 2: 9b_est2: * 3: 9b_hcc: * 4: 9b_est3: * 5: 9b_est4: * 6: 9b_est5: * 7: 9b_est6: * 8: 9b_gss1: * 9: 9b_gss2: *	BI261161 BI261161 BI261161 BI261161 BI261161					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		AAS22689 AAS22689 AAS22689 AAS22689 AAS22689					
SUMMARIES	%	CN78116 CN78116 CN78116 CN78116 CN78116					
result	No.	Score	Match	Length	DB	ID	Description
1	44	24.9	786	7	CN147592	CN147592	WOUND1_50_E10_91_A002 Wounded leaves Sorghum bicolor cDNA clone
2	43.2	24.4	632	2	CN147592	CN147592	WOUND1_50_E10_A002 5' mRNA sequence.
3	42.6	24.1	466	7	CN147592	CN147592	EST.
4	42.6	24.1	684	7	CN147592	CN147592	Sorghum bicolor (sorghum)
5	42.2	23.7	778	4	CN147592	CN147592	Bakteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
6	40.4	22.8	446	5	CN147592	CN147592	1 (bases 1 to 786)
7	40.4	22.8	513	5	CN147592	CN147592	Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Brady, J., Eastman, A., Miller, V., Gonzalez, M., Antuso, C., Chhabra, D., Johnson, H., Kamran, D. and Pratt, L.H.
8	40.4	22.8	571	4	CN147592	CN147592	A Sorghum EST database: mechanically damaged and methyl jasmonate-treated leaves
9	40.4	22.8	617	6	CN147592	CN147592	Unpublished (2003)
10	40.4	22.8	620	6	CN147592	CN147592	Other ESTs: WOUND1_50_E10_B1_A002
11	40.4	22.8	624	5	CN147592	CN147592	Contact: Cordonnier-Pratt MM
12	40.4	22.8	624	5	CN147592	CN147592	Laboratory for Genomics and Bioinformatics
13	40.4	22.8	652	5	CN147592	CN147592	The University of Georgia, Department of Plant Biology
14	40.4	22.8	666	6	CN147592	CN147592	Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
15	40.4	22.8	668	6	CN147592	CN147592	Te: 706 542 1860
16	40.4	22.8	694	7	CN147592	CN147592	Fax: 706 583 0210
17	40.4	22.8	702	6	CN147592	CN147592	Email: mpratt@uga.edu
18	40.4	22.8	780	7	CN147592	CN147592	Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
19	40.4	22.8	834	6	CN147592	CN147592	the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
20	40.4	22.8	835	6	CN147592	CN147592	Seq primer: Sug5 (CTTCGCTCTAAAAGCTGCG).
21	40.4	22.8	886	6	CN147592	CN147592	Location/Qualifiers
22	40.4	22.8	1122	3	CN147592	CN147592	Source 1 - 786
23	39.8	22.5	1080	6	CN147592	CN147592	/organism="Sorghum bicolor"
24	39.8	22.5	201	1	CN147592	CN147592	/mol type="mRNA"
					CN147592	CN147592	/cuiEvvar="BTx623"
					CN147592	CN147592	/db_xref="taxon:4558"
					CN147592	CN147592	/clone="WOUND1_50_E10_A002"
					CN147592	CN147592	/lab_host="DHLB-T1 phage-resistant E. coli"
					CN147592	CN147592	/clone_1lb="Wound leaves"
					CN147592	CN147592	/note="Organ: Leaf; Vector: PME18S-FL3; Site 1: XbaI;

Site 2: XhoI: The library was prepared from polyA+ RNA harvested from 8-day-old hydroponically grown, BtX623 sorghum seedlings. For some plants, one-half of the second leaf was crushed without damaging the midvein. For others, methyl jasmonate was added to the growth medium to a final concentration of 100 μ M. Leaves were harvested 3 and 27 h after treatment and pooled. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pMBE18S-F13 vector (5'-prime DraIII site is CACTGTC, 3'-prime DraIII site is CACCATGTG). XbaI excises the cDNA insert.¹¹

Note: this is a NIH MGC Library."

		Note: this is a NIH_MGC Library."
Site 2: XhoI; The library was prepared from polyA+ RNA harvested from 8-day-old hydroponically grown, BTx623 sorghum seedlings. For some plants, one-half of the second leaf was crushed without damaging the midrib. For others, methyl jasmonate was added to the growth medium to a final concentration of 100 uM. Leaves were harvested 3 and 27 hr after treatment and pooled. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FL3 vector (5-prime DraIII site is CACTGTTGTC, 3-prime DraIII site is CACCATGTC). XhoI excises the cDNA insert."	ORIGIN	
	Query Match 24.9%; Score 44; DB 7; Length 786;	
Best Local Similarity 57.1%; Pred. No. 0.12; Gaps 0;	Best Local Similarity 54.4%; Pred. No. 0.19; Gaps 0;	
Matches 80; Conservative 0; Mismatches 60; Indels 0; Gaps 0;	Matches 87; Conservative 0; Mismatches 73; Indels 0; Gaps 0;	
Qy 30 CAGCTCGACAAACACCTAACCTTGCGTACCCCTGGGGACACANCCGGACTCATCAAGAT 89	Qy 1 GCGGACGTGTCAGGGAACTACCCCTGGACAGCTGGACATCAGATCTGGGACCC 60	Qy 61 CTGGGGCAGAACCCGGACTGTCATCAAGAGCTGGCAAGAACCTGCGGACTGCACTGGCTACCCCTAC 120
Db 350 CGCGGGGACAACTCAACCTAACCTGGGGACATCGGCCATCTGGCTGAGACAGCTCAAGAC 409	Db 244 CTGGCTTACTACTAGACAGAACATCATGAGAACAGGAGGCTGGCCAGGCGCC 343	Db 304 CGGTTCGACTTCCAGGGCTGGGCCAGGSCCTGCGAC 343
Qy 90 CTGCCAGAAGCAGGGCTGACTACGGCTACTACGGCTACGGCTACGGCTGGGAGCTGAGT 149	Qy 121 TGCTAGCGCTTCAGTGTGGAGTCTGAGAG 160	Qy 62 CF846529 466 bp mRNA linear EST 30-OCT-2003
Db 410 CCTCTCTACTCCGACTTTCGSGGAGAACATCTCTGTCGGGACAGGCTGGGTTCGAGTC 469	DEFINITION pHB038XO20f USDA-IRAFS:Expression of Phytophthora sojae genes during infection and propagation_SHB Phytophthora sojae cDNA clone SHB038O20 5, mRNA sequence.	Db 304 CF846529 1 GI:38062183
Qy 150 CCTGAAGGACGAGAACCTCA 169	ACCESSION CF846529	VBI
Db 470 CATCATCCAGCCATGGCA 489	VERSION	1880 Pratt Dr., Blacksburg, VA 24061, USA
	KEYWORDS	Email: 540-231-7319
	SOURCE	PCR Primers
	ORGANISM	Phytophthora sojae
		Eukaryota; Stramenopiles; Oomycetes; Pythiales; Pythiaceae;
		Phytophthora.
	REFERENCE 1 (bases 1 to 466)	1. 466
	AUTHORS Tyler, B.	/organism="Phytophthora sojae"
	TITLE	/mol type="mRNA"
	JOURNAL	/db_Xref="Taxon_67593"
	COMMENT	/clone="SHB038O20"
		/tissue type="mycelium"
		/cell_line="P6497"
		/dev_stage="48 hr. post infection stage"
		/lab_host="Soybean plant"
		/clone_lib="USDA-IRAFS:Expression of Phytophthora sojae genes during infection and propagation_SHB"
		/note="vector: PBK-CMV, Site_1: EcoRI, Site_2: XbaI"
RESULT 2 BE262829	FEATURES source	ORIGIN
LOCUS BE262829	EST 26-OCT-2000	
DEFINITION 601151586P1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3507620 5', mRNA sequence.		
VERSION BE262829		
ESTR. BE262829.1 GI:9136188		
SOURCE Homo sapiens (human)		
ORGANISM Homo sapiens		
REFERENCE 1 (bases 1 to 632)		
AUTHORS Tissue Procurement: ARCC		
CDNA Library Preparation: Ling Hong/Rubin Laboratory		
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)		
DNA Sequencing by: Incyte Genomics, Inc.		
Unpublished (1999)		
CONTACT: Robert Strausberg, Ph.D.		
Email: cgsbs-r@mail.nih.gov		
Tissue Procurement: ARCC		
CDNA Library Preparation: Ling Hong/Rubin Laboratory		
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)		
DNA Sequencing by: Incyte Genomics, Inc.		
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at: image.liln.gov		
Plate: LUCM187 row: 1 column: 21		
High quality sequence start: 27		
High quality sequence stop: 616.		
Location/Qualifiers 1..632		
/organism="Homo sapiens"		
/mol type="mRNA"		
/db_Xref="taxon:9606"		
/clone IMAGE:3507620"		
/tissue type="neuroblastoma"		
/lab_host="DH10B (phage-resistant)"		
/clone lib="NIH_MGC_19"		
/note="Organ: brain; Vector: P0TB7; Site 1: XbaI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5'-adaptor: GCGCAAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP cDNA synthesis kit (Stratagene) and SuperScript II RT (Life Technologies).		
RESULT 2 BE262829	FEATURES source	ORIGIN
LOCUS BE262829	EST 26-OCT-2000	
DEFINITION 601151586P1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3507620 5', mRNA sequence.		
VERSION BE262829		
ESTR. BE262829.1 GI:9136188		
SOURCE Homo sapiens (human)		
ORGANISM Homo sapiens		
REFERENCE 1 (bases 1 to 632)		
AUTHORS Tissue Procurement: ARCC		
CNA Library Preparation: Ling Hong/Rubin Laboratory		
CNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)		
DNA Sequencing by: Incyte Genomics, Inc.		
Unpublished (1999)		
CONTACT: Robert Strausberg, Ph.D.		
Email: cgsbs-r@mail.nih.gov		
Tissue Procurement: ARCC		
CNA Library Preparation: Ling Hong/Rubin Laboratory		
CNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)		
DNA Sequencing by: Incyte Genomics, Inc.		
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at: image.liln.gov		
Plate: LUCM187 row: 1 column: 21		
High quality sequence start: 27		
High quality sequence stop: 616.		
Location/Qualifiers 1..632		
/organism="Homo sapiens"		
/mol type="mRNA"		
/db_Xref="taxon:9606"		
/clone IMAGE:3507620"		
/tissue type="neuroblastoma"		
/lab_host="DH10B (phage-resistant)"		
/clone lib="NIH_MGC_19"		
/note="Organ: brain; Vector: P0TB7; Site 1: XbaI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5'-adaptor: GCGCAAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP cDNA synthesis kit (Stratagene) and SuperScript II RT (Life Technologies).		
RESULT 2 BE262829	FEATURES source	ORIGIN
LOCUS BE262829	EST 26-OCT-2000	
DEFINITION 601151586P1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3507620 5', mRNA sequence.		
VERSION BE262829		
ESTR. BE262829.1 GI:9136188		
SOURCE Homo sapiens (human)		
ORGANISM Homo sapiens		
REFERENCE 1 (bases 1 to 632)		
AUTHORS Tissue Procurement: ARCC		
CNA Library Preparation: Ling Hong/Rubin Laboratory		
CNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)		
DNA Sequencing by: Incyte Genomics, Inc.		
Unpublished (1999)		
CONTACT: Robert Strausberg, Ph.D.		
Email: cgsbs-r@mail.nih.gov		
Tissue Procurement: ARCC		
CNA Library Preparation: Ling Hong/Rubin Laboratory		
CNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)		
DNA Sequencing by: Incyte Genomics, Inc.		
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at: image.liln.gov		
Plate: LUCM187 row: 1 column: 21		
High quality sequence start: 27		
High quality sequence stop: 616.		
Location/Qualifiers 1..632		
/organism="Homo sapiens"		
/mol type="mRNA"		
/db_Xref="taxon:9606"		
/clone IMAGE:3507620"		
/tissue type="neuroblastoma"		
/lab_host="DH10B (phage-resistant)"		
/clone lib="NIH_MGC_19"		
/note="Organ: brain; Vector: P0TB7; Site 1: XbaI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5'-adaptor: GCGCAAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP cDNA synthesis kit (Stratagene) and SuperScript II RT (Life Technologies).		

REFERENCE		FEATURES	Plate: 946120 row: G column: 01.
AUTHORS	1 (bases 1 to 446)	source	Location/Qualifiers 1. .513
TITLE	Maize ESTs from various cDNA libraries sequenced at Stanford University		/organism="Zea mays" 'mol type="mRNA'" 'cultivar="OH43'" 'db_xref="taxon:45777'" 'tissue_type="cassels"' 'dev_stage="just after the transition from vegetative to inflorescence development"' 'lab_host="XLOLR'" 'clone_lib="946 - tassel primordium prepared by Schmidt lab"' 'note="Organ: tassels; Vector: HybrizAP; Site_1: ECORI; Site_2: XbaI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybrizAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."'
COMMENT	Unpublished (1999)		
CONTACT	Walbot V		
DEPARTMENT	Department of Biological Sciences		
STANFORD UNIVERSITY	855 California Ave, Palo Alto, CA 94304, USA		
TEL	650 723 2227		
FAX	650 725 8221		
EMAIL	walbot@stanford.edu		
PLATE	1091028 row: H column: 08.		
LOCATION/QUALIFIERS	1. .446		
	/organism="Zea mays"		
	'mol type="mRNA'"		
	'cultivar="OH43'"		
	'db_xref="taxon:45777'"		
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	'dev_stage="10.5 cm to 2 cm"'		
	'lab_host="Stratagene XLOLR'"		
	'clone_lib="1091 - Immature ear with common ESTs screened by Schmidt lab"'		
	'note="Organ: Immature ear; Vector: PAD-GAL4; Site_1: EcoRI; Site_2: XbaI; RNA from library 606 was filtered for common ESTs found in 606."'		
ORIGIN			
QUERY MATCH	22.8%; Score 40.4; DB 5; Length 513;		
BEST LOCAL SIMILARITY	54.8%; Pred. No. 1.1;		
MATCHES	80; Conservative 0; Mismatches 66; Indels 0; Gaps 0;		
QY	29 ACACCTGGACAACGCTTACCTGTGGCACCCTGGGACACCCGGACTGCGATCAAGA 88		
DB	123 ACAAGGTGTACAAGGGCACCTGTGACAACGGCTGGCGTCACCGGCCATCTGGTGC 182		
RESULT 8			
LOCUS	BT1478941		
DEFINITION	94907107.y1 949 - Juvenile leaf and shoot cDNA from Steve Moose		
ACCESSION	BT1478941		
VERSION	BT1478941.1		
SOURCE	EST.		
ORGANISM	Zea mays		
EUKARYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD Clade; Panicoideae; Andropogoneae; Zea.			
REFERENCE	94907107.y1		
AUTHORS	Walbot, V.		
TITLE	Maize ESTs from various cDNA libraries sequenced at Stanford University		
COMMENT	Unpublished (1999)		
CONTACT	Walbot V		
DEPARTMENT	Department of Biological Sciences		
STANFORD UNIVERSITY	855 California Ave, Palo Alto, CA 94304, USA		
TEL	650 723 2227		
FAX	650 725 8221		
EMAIL	walbot@stanford.edu		
PLATE	945071 row: B column: 07.		
FEATURES			
SOURCE	1. .571		
	/organism="Zea mays"		
	'mol type="mRNA'"		
	'cultivar="W64A"'		
	'db_xref="taxon:45777'"		
	'tissue_type="immature leaf primordium and vegetative meristem"'		
	'dev_stage="4 stages from 3-13 days after imbibing"'		
	'lab_host="E. coli XLOLR"'		
RESULT 7			
LOCUS	BQ779473		
DEFINITION	946120G01.y1 946 - tassel primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.		
ACCESSION	BQ779473		
VERSION	BQ779473.1		
KEYWORDS	GI:21987945		
SOURCE	EST.		
ORGANISM	Zea mays		
EUKARYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD Clade; Panicoideae; Andropogoneae; Zea.			
REFERENCE	1 (bases 1 to 513)		
AUTHORS	Walbot, V.		
TITLE	Maize ESTs from various cDNA libraries sequenced at Stanford University		
COMMENT	Unpublished (1999)		
CONTACT	Walbot V		
DEPARTMENT	Department of Biological Sciences		
STANFORD UNIVERSITY	855 California Ave, Palo Alto, CA 94304, USA		
TEL	650 723 2227		
FAX	650 725 8221		
EMAIL	walbot@stanford.edu		

/clone_lib="949 - Juvenile leaf and shoot cDNA from Steve Moose"
 /note="Organ: juvenile vegetative shoots; Vector: pAD-GAL4-2.1; Site 1: EcoRI; Site 2: XhoI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI ('S') and XhoI ('3') directional cloning into Lambda Hybrizap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."

ORIGIN

Query Match Score 40.4; DB 4; Length 571;
 Best Local Similarity 22.8%; Pred. No. 1.1;
 Matches 80; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 29 ACAGCTCGGACAACACTTACCTGGGACAAACCCGACTGCACTAACAGA 88
 Db 251 ACAAGGTGTCAACCGGAGCTGGCAAGGGCTGGCTACCCGGGATCTGGTC 310

Qy 89 TCTGCCAGAAGCACGGCTGACTACGGCTACTGCTACCGTTCCAGTTGGGACT 148
 Db 311 TCATCCAGCAGTCCCAGACGGCAACGGGACCCGTTACGGGCCATCTACAGCTTCTACT 370

Qy 149 TCTCTGAAGGACGGAGACGTGAGGT 174
 Db 371 TCGGAGACTACGGGCCACATCTCGGTG 396

RESULT 9
 CAB828471 617 bp mRNA linear EST 11-DEC-2002
 DEFINITION 1114028F02.Y3 1114 - Unigene IV from Maize Genome Project Zea mays
 cDNA, mRNA sequence.

ACCESSION CAB828471
 VERSION CAB828471.1
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; PACCAD clade; Panicoideae; Andropogonae; Zea.

REFERENCE Walbot, V.
 AUTHORS Walbot, V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
 Unpublished (1999)
 Contact: Walbot, V.
 Department of Biological Sciences
 Stanford University
 855 California Ave., Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 3529_1 95_1 row: F column: 01.

FEATURES Source
 /db_xref="taxon:577"
 /tissue_type="ear"
 /dev_stage="2 mm"
 /lab_host="E. coli XLOR"
 /clone_lib="3529 - 2 mm ear tissue from Schmidt and Hake labs"
 /note="organ: ear; Vector: PAD-GAL4-2.1; Site 1: EcoRI; Site 2: XhoI; RNA isolated by Hake lab, 1 million pfu amplified. Ampicillin is the selection marker."

ORIGIN

Query Match Score 40.4; DB 6; Length 620;
 Best Local Similarity 22.8%; Pred. No. 1.1;
 Matches 80; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
 /db_xref="dbEST:1091028H08.Y2"
 /db_xref="dbEST:4577"
 /clone_lib="1114 - Unigene IV from Maize Genome Project"
 /note="This library represents the unique genes found in the fourth round of EST sequencing at Stanford University for the maize genome project. Sequences are present from libraries 1091 and 3524. Contigs were assembled using ZmDBAssembler and 2 representatives from each contig were selected for the Unigene set. All singlets were also

selected."

ORIGIN

Query Match Score 40.4; DB 6; Length 617;
 Best Local Similarity 54.8%; Pred. No. 1.1;
 Matches 80; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
 Qy 29 ACAGCTCGGACAACACTTACCTGGGACAAACCCGACTGCACTAACAGA 88
 Db 327 ACAAGGTGTACACGGCTGACAAAGGGCTACCCGGGATCTCGGTGC 386
 Qy 89 TCTGCCAGAAGCACGGCTGACTACGGCTACTGCTACCGTTCCAGTTGGTGGGAGT 148
 Db 387 TCATCCAGCAGTCCCAGCAGACGGGACCCGATCTACAGCTTCTACT 446
 Qy 149 TCCCTGAAGGACGGAGAACGTGAAAGTG 174
 Db 447 TCGGAGACTACGGCACATCTCGGTG 472

RESULT 10
 LOCUS CB886436_C
 DEFINITION 3529_1 95_1_F01.x_1 3529 - 2 mm ear tissue from Schmidt and Hake labs Zea mays cDNA, mRNA sequence.

ACCESSION CB886436
 VERSION CB886436.1
 KEYWORD EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; PACCAD clade; Panicoideae; Andropogonae; Zea.

REFERENCE Walbot, V.
 AUTHORS Walbot, V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
 Unpublished (1999)
 Contact: Walbot, V.
 Department of Biological Sciences
 Stanford University
 855 California Ave., Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 3529_1 95_1 row: F column: 01.

FEATURES Source
 /db_xref="taxon:577"
 /tissue_type="ear"
 /dev_stage="2 mm"
 /lab_host="E. coli XLOR"
 /clone_lib="3529 - 2 mm ear tissue from Schmidt and Hake labs"
 /note="organ: ear; Vector: PAD-GAL4-2.1; Site 1: EcoRI; Site 2: XhoI; RNA isolated by Hake lab, 1 million pfu amplified. Ampicillin is the selection marker."

ORIGIN

Query Match Score 40.4; DB 6; Length 620;
 Best Local Similarity 54.8%; Pred. No. 1.1;
 Matches 80; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 29 ACAGCTCGGACAACACTTACCTGGGACAAACCCGACTGCACTAACAGA 88
 Db 544 ACAAGGTGTACACGGCTGACCCGAGCTGZGAAGGGCTACCCGGGATCTCGGTGC 485
 Qy 89 TCTGCCAGAAGCACGGCTGACTACGGCTACTGCTACCGTTCCAGTTGGTGGGAGT 148
 Db 484 TCATCCAGCAGTCCCAGCAGACGGGACCCGATCTACAGCTTCTACT 425

JOURNAL University Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Fax: 650 725 2227
 Email: walbot@stanford.edu

FEATURES source

Plate: 946134 row: C column: 03.
 Location/Qualifiers 1 .652
 /organism="Zea mays"
 /mol type="mRNA"
 /cultivar="OH43"
 /db_xref="taxon:4577"
 /tissue type="tassels"
 /dev stage="just after the transition from vegetative to inflorescence development"
 /lab_host="XLOLR"
 /clone_lib="946 - tassel primordium prepared by Schmidt lab"
 /note="Organ: tassels; Vector: HybriZAP; Site_1: ECORI; Site_2: XbaI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybriZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."

ORIGIN

Query Match	22 .8%	Score 40 .4;	DB 5;	Length 666;
Best Local Similarity	54 .8%	Pred. No. 1.1;		
Matches	80;	Conservative	0;	Mismatches 0;
Indels	66;			Gaps 0;

Qy 29 ACAGGTGGACAAACACTACCTGTCGACCCCTGGGACAACCGGGACTGCATCAAGA 88
 Db 331 ACAAGTGTAAACGGCTGTCGACAAAGGGCTGGCTCACCGGGCATCTCGTGC 390
 Qy 89 TCTGCAGAGCAGGCCGCTGACTACGGTCACTGCTACGGTTCAAGTGTGGTGCGAGT 148
 Db 391 TCATCAGGACAGTCGCCGACATCTCGTCTACAGCTCTACAGCTCTACT 450

ORIGIN

Query Match	22 .8%	Score 40 .4;	DB 5;	Length 652;
Best Local Similarity	54 .8%	Pred. No. 1.1;		
Matches	80;	Conservative	0;	Mismatches 66;
Indels	66;			Gaps 0;

Qy 29 ACAGCTGGACAAACCTAACGTGCGAACCCGGACTGCATCAAGA 88
 Db 360 ACAAAGTGTAAACGGAGCTGGGAGCTGGCAAGGGCTGGGTACCGGGCATCTGGTC 419
 Qy 89 TCTGCAGAGCAGCACGGCTGACTACGGTCACTGCTGGTGGCTACCGGGCATCTGGTC 419
 Db 420 TCATCAGGACAGTCGCCGACGGGACCCGCTACGGCCATCTACAGCTCTACT 479

RESULT 15

LOCUS	CD001260	668 bp mRNA linear EST 01-MAY-2003
DEFINITION	3529_1_95_1_F01_Y1	3529 - 2 mm ear tissue from Schmidt and Hake
ACCESSION	CD001260	labs Zea mays cDNA, mRNA sequence.
VERSION	CD001260.1	EST.
KEYWORDS		SOURCE
ORGANISM		zea mays
		Eukaryota; Viridiplantae; Streptophytta; Embryophytta; Tracheophyta; Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE CD001260

AUTHORS Walbot, V.

TITLE Unpublished (1999)

JOURNAL Department of Biological Sciences

COMMENT Stanford University
 955 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 725 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu

PLATE: 3529_1_95_1 row: F column: 01.

FEATURES source

RESULT 14

LOCUS BU499682 666 bp mRNA linear EST 12-SEP-2002

DEFINITION 946178C07 .Y1 946 - tassel primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.

ACCESSION BU499682

VERSION BU499682.1 GI:22819592

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

COMMENT Maize ESTs from various cDNA libraries sequenced at Stanford University

REFERENCE Unpublished (1999)

AUTHORS Contact: Walbot V

TITLE Department of Biological Sciences

COMMENT Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227

PLATE: 650 725 8221

FEATURES source

RESULT 13

LOCUS BU499682 666 bp mRNA linear EST 12-SEP-2002

DEFINITION 946178C07 .Y1 946 - tassel primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.

ACCESSION BU499682

VERSION BU499682.1 GI:22819592

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

COMMENT Maize ESTs from various cDNA libraries sequenced at Stanford University

REFERENCE Unpublished (1999)

AUTHORS Contact: Walbot V

TITLE Department of Biological Sciences

COMMENT Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227

PLATE: 650 725 8221

FEATURES source

RESULT 12

LOCUS BU499682 666 bp mRNA linear EST 12-SEP-2002

DEFINITION 946178C07 .Y1 946 - tassel primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.

ACCESSION BU499682

VERSION BU499682.1 GI:22819592

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

COMMENT Maize ESTs from various cDNA libraries sequenced at Stanford University

REFERENCE Unpublished (1999)

AUTHORS Contact: Walbot V

TITLE Department of Biological Sciences

COMMENT Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227

PLATE: 650 725 8221

FEATURES source

RESULT 11

LOCUS BU499682 666 bp mRNA linear EST 12-SEP-2002

DEFINITION 946178C07 .Y1 946 - tassel primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.

ACCESSION BU499682

VERSION BU499682.1 GI:22819592

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

COMMENT Maize ESTs from various cDNA libraries sequenced at Stanford University

REFERENCE Unpublished (1999)

AUTHORS Contact: Walbot V

TITLE Department of Biological Sciences

COMMENT Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227

PLATE: 650 725 8221

FEATURES source

RESULT 10

LOCUS BU499682 666 bp mRNA linear EST 12-SEP-2002

DEFINITION 946178C07 .Y1 946 - tassel primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.

ACCESSION BU499682

VERSION BU499682.1 GI:22819592

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

COMMENT Maize ESTs from various cDNA libraries sequenced at Stanford University

REFERENCE Unpublished (1999)

AUTHORS Contact: Walbot V

TITLE Department of Biological Sciences

COMMENT Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227

PLATE: 650 725 8221

FEATURES source

RESULT 9

LOCUS BU499682 666 bp mRNA linear EST 12-SEP-2002

DEFINITION 946178C07 .Y1 946 - tassel primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.

ACCESSION BU499682

VERSION BU499682.1 GI:22819592

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

COMMENT Maize ESTs from various cDNA libraries sequenced at Stanford University

REFERENCE Unpublished (1999)

AUTHORS Contact: Walbot V

TITLE Department of Biological Sciences

COMMENT Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227

PLATE: 650 725 8221

FEATURES source

RESULT 8

LOCUS BU499682 666 bp mRNA linear EST 12-SEP-2002

DEFINITION 946178C07 .Y1 946 - tassel primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.

ACCESSION BU499682

VERSION BU499682.1 GI:22819592

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

COMMENT Maize ESTs from various cDNA libraries sequenced at Stanford University

REFERENCE Unpublished (1999)

AUTHORS Contact: Walbot V

TITLE Department of Biological Sciences

COMMENT Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227

PLATE: 650 725 8221

FEATURES source

RESULT 7

LOCUS BU499682 666 bp mRNA linear EST 12-SEP-2002

DEFINITION 946178C07 .Y1 946 - tassel primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.

ACCESSION BU499682

VERSION BU499682.1 GI:22819592

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

COMMENT Maize ESTs from various cDNA libraries sequenced at Stanford University

REFERENCE Unpublished (1999)

AUTHORS Contact: Walbot V

TITLE Department of Biological Sciences

COMMENT Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227

PLATE: 650 725 8221

FEATURES source

RESULT 6

LOCUS BU499682 666 bp mRNA linear EST 12-SEP-2002

DEFINITION 946178C07 .Y1 946 - tassel primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.

ACCESSION BU499682

VERSION BU499682.1 GI:22819592

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

COMMENT Maize ESTs from various cDNA libraries sequenced at Stanford University

REFERENCE Unpublished (1999)

AUTHORS Contact: Walbot V

TITLE Department of Biological Sciences

COMMENT Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227

PLATE: 650 725 8221

FEATURES source

RESULT 5

LOCUS BU499682 666 bp mRNA linear EST 12-SEP-2002

DEFINITION 946178C07 .Y1 946 - tassel primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.

ACCESSION BU499682

VERSION BU499682.1 GI:22819592

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

COMMENT Maize ESTs from various cDNA libraries sequenced at Stanford University

REFERENCE Unpublished (1999)

AUTHORS Contact: Walbot V

TITLE Department of Biological Sciences

COMMENT Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227

PLATE: 650 725 8221

FEATURES source

RESULT 4

LOCUS BU499682 666 bp mRNA linear EST 12-SEP-2002

DEFINITION 946178C07 .Y1 946 - tassel primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.

ACCESSION BU499682

VERSION BU499682.1 GI:22819592

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

COMMENT Maize ESTs from various cDNA libraries sequenced at Stanford University

REFERENCE Unpublished (1999)

AUTHORS Contact: Walbot V

TITLE Department of Biological Sciences

COMMENT Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227

PLATE: 650 725 8221

FEATURES source

RESULT 3

LOCUS BU499682 666 bp mRNA linear EST 12-SEP-2002

DEFINITION 946178C07 .Y1 946 - tassel primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.

ACCESSION BU499682

VERSION BU499682.1 GI:22819592

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

COMMENT Maize ESTs from various cDNA libraries sequenced at Stanford University

REFERENCE Unpublished (1999)

AUTHORS Contact: Walbot V

TITLE Department of Biological Sciences

COMMENT Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227

PLATE: 650 725 8221

FEATURES source

RESULT 2

LOCUS BU499682 666 bp mRNA linear EST 12-SEP-2002

DEFINITION 946178C07 .Y1 946 - tassel primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.

ACCESSION BU499682

VERSION BU499682.1 GI:22819592

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

COMMENT Maize ESTs from various cDNA libraries sequenced at Stanford University

REFERENCE Unpublished (1999)

AUTHORS Contact: Walbot V

TITLE Department of Biological Sciences

COMMENT Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227

PLATE: 650 725 8221

FEATURES source

RESULT 1

LOCUS BU499682 666 bp mRNA linear EST 12-SEP-2002

DEFINITION 946178C07 .Y1 946 - tassel primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.

ACCESSION BU499682

VERSION BU499682.1 GI:22819592

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

COMMENT Maize ESTs from various cDNA libraries sequenced at Stanford University

REFERENCE Unpublished (1999)

AUTHORS Contact: Walbot V

TITLE Department of Biological Sciences

COMMENT Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227

PLATE: 650 725 8221

FEATURES source

Site 2: XbaI; RNA isolated by Hake lab. 1 million pfu
amplified. Ampicillin is the selection marker."

ORIGIN

Query	Match	Score	404;	DB	6;	Length	668;
Best	Local	Similarity	22.8%;	Pred.	No	1..1;	
Matches	80;	Conservative	54.8%;	Mismatches	0;	Indels	0;
				Gaps	0;		
Qy	29	ACAGCTGGACAAACCCATACCTGTCGACACCCCTGGCAACCCGACTGCATCAGA	88				
Db	373	ACAGGTGTACAACGGCACCCCTGGACAACGGCTGGGCTCACCGCGGCAATGCGTGC	432				
Qy	89	TCTGCCAGAAGCACGGCTGACTAACGGCTACTACGCTGACTGCTACCGTTCAGTTGGTGCGAGT	148				
Db	433	TCATCGAGACGTCGCCGACGGACCCCTACAGGCACTAACGGCATCTACAGCTTCTACT	492				
Qy	149	TCCCTGAAGGACGAGAACGTCAGGTG	174				
Db	493	TCGGAGACTAACGGCACATCTCGSTG	518				

Search completed: July 30, 2005, 20:16:27
Job time : 1947.04 secs

Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6						
OM nucleic - nucleic search, using sw model							
Run on:	July 30, 2005, 15:39:09 ; Search time 1277.13 Seconds (without alignment) 6791.361 Million cell updates/sec						
Title:	US-10-617-978-14_COPY_62_240						
Perfect score:	179						
Sequence:	1 cggctacgtccggaaac.....atggaaacctggaaaggctctga 179						
Scoring table:	IDENTITY_NUC						
Searched:	Gapop 10.0 , Gapext 1.0						
Total number of hits satisfying chosen parameters:	9416466						
Minimum DB seq length:	0						
Maximum DB seq length:	2000000000						
Post-processing:	Minimum Match 0% Maximum Match 100%						
	Listing first 45 summaries						
Database :	GenEmbl: 1: gb_ba:/* 2: gb_hdg:/* 3: gb_ni:/* 4: gb_om:/* 5: gb_ov:/* 6: gb_dat:/* 7: gb_bh:/* 8: gb_dl:/* 9: gb_pr:/* 10: gb_ro:/* 11: gb_sts:/* 12: gb_sy:/* 13: gb_un:/* 14: gb_vl:/*						
Result No.	Score	Query	Match	Length	DB	ID	Description
-	-	-	-	-	-	-	-
1	57.2	32.0	354	3	AF151798		AF151798 Mesobuthus martensii insect beta-neurotoxin (bct) mRNA, complete cds.
2	57.2	32.0	469	3	AY282464		AY282464 Mesobuthus martensii Sequence
3	42.2	23.6	270	6	AR566415		AR566415 Sequence
4	42.2	23.6	270	6	AR061772		AR061772 Sequence
5	40.8	22.8	270	6	AR566414		AR566414 Sequence
6	40.8	22.8	270	6	AR566416		AR566416 Sequence
7	40.8	22.8	270	6	AR061770		AR061770 Sequence
8	40.8	22.8	270	6	AX061774		AX061774 Sequence
9	38	21.2	270	6	AR566413		AR566413 Sequence
10	38	21.2	270	6	AX061768		AX061768 Sequence
11	38	21.2	316	3	AF491133		AF491133 Centruroid
12	36.8	20.6	192	3	AY351304		AY351304 Centruroid
13	36.8	20.6	192	3	AY351305		AY351305 Centruroid
14	36.8	20.6	192	3	AY351306		AY351306 Centruroid
15	36.8	20.6	192	3	AY351307		AY351307 Centruroid
16	36.8	20.6	319	3	AF338459		AF338459 Centruroid
17	36.8	20.6	320	3	AF338461		AF338461 Centruroid
18	36.8	20.6	323	3	AF338454		AF338454 Centruroid
19	36.8	20.6	323	3	AF338455		AF338455 Centruroid

/gene="bt"
 /note="BmKBR2"
 /codon_start=1
 /product="insect beta neurotoxin"
 /protein_id="AAP1418_2"
 /db_xref="GI:53828930"
 /translation="MMKKFLFSEMVILFSIANGSIRSIRGDDPGNYPNTAYGNKYCTLG
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ORIGIN

Query Match 32.0%; Score 57.2; DB 3; Length 354;
 Best Local Similarity 58.0%; Pred. No. 1.2e-07;
 Matches 101; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 6 GACGTCCCCGGAAACTACCACATGATTTCGGACATAACCTTCCGACAAATACCTACCTGTGGCCCTTTG 65
 Db 81 GACCATCAGGAATTATCGACAATGGTTACGGTACCAAATTATGTAGATTTG 140

Qy 66 GGAGATAATCCGGACTGCATTANGATCTGTCAGAAAACGGTGGATTACGGGTATTCG 125
 Db 141 GGAGAAAATGAATTGGAAATATTTAATTGCAATGGAGTTACTATGGTTATTGT 200

Qy 126 TACGCCCTCAATCTGGTGTGAAGATGAAACGTGAAGCTGA 179
 Db 201 TACAATTCCAGATSTTGTGCGAAAAATTGGAGATAAAGACGTACCAATTGA 254

RESULT 3 AR566415
 LOCUS AR566415
 DEFINITION Sequence 34 from patent US 6768002.
 ACCESSION AR566415
 VERSION AR566415.1 GI:53983405
 KEYWORDS Unknown.
 SOURCE Unclassified.
 ORGANISM Herrmann, R. and Wong, J.F.
 REFERENCE 1 (bases 1 to 270)
 AUTHORS Herrmann, R. and Wong, J.F.
 TITLE Scorpion toxins
 JOURNAL Patent: US 6768002-A 34 27-JUL-2004;
 FEATURES Location/Qualifiers
 source 1. .270
 /organism="unknown"
 /mol_type="genomic DNA"
 ORIGIN

Query Match 23.6%; Score 42.2; DB 6; Length 270;
 Best Local Similarity 61.3%; Pred. No. 0.011;
 Matches 68; Conservative 0; Mismatches 0;
 Gaps 0;

Qy 67 GAGATAATCCGGACTGCATTAGATCTGTCAGAAAACGGTGGATTACGGGTATTCG 126
 Db 128 GGTACATGATATTGTCGGACATTTGTAAGTACATGGAGTGAAATTGGGTATTTT 187

Qy 127 ACGCTTCCAATGCTGGTGTGAATTCTGAAGGTGAAACGTGAAGTCT 177
 Db 188 GGGTACCTCGTGTGGTGTGAATTGGAGAACATCAATT 238

RESULT 4 AX061772
 LOCUS AX061772
 DEFINITION Sequence 34 from patent WO0078957.
 ACCESSION AX061772
 VERSION AX061772.1 GI:12539858
 KEYWORDS Hottentotta judaica
 SOURCE Hottentotta judaica
 ORGANISM Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; Buthoidea; Buthidae; Mesobuthus
 KEYWORD SOURCE Hottentotta judaica
 ORGANISM Buthoidea; Buthidae; Hottentotta.

REFERENCE 1
 AUTHORS Herrmann, R., Lee, J.M. and Wong, J.F.
 TITLE Scorpion toxins from buthotus judaicus
 JOURNAL Patent: WO 0078957-A 34 28-DEC-2000;
 E.I. DU PONT DE NEMOURS AND COMPANY (US)
 Location/Qualifiers
 source 1. .270
 /organism="Hottentotta judaica"
 /mol_type="unassigned DNA"
 /db_xref="Taxon:6863"

ORIGIN

Query Match 23.6%; Score 42.2; DB 6; Length 270;
 Best Local Similarity 61.3%; Pred. No. 0.011;
 Matches 68; Conservative 0; Mismatches 43;
 Indels 0; Gaps 0;

Qy 67 GAGATAATCCGACTGCAATTAAAGATCTGTGAGAACACGGTGTGGATTACGGTATTGGT 126
 Db 128 GTGAICATGATTATGTCGGACATTGTAAGTACATGAAATTGGPATTTGTT 187

RESULT 5
 LOCUS AR566414 DEFINITION Sequence 32 from patent US 6768002. DNA linear PAT 08-OCT-2004
 ACCESSION AR566414
 VERSION AR566414.1 GI:53983404
 KEYWORDS Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED
 REFERENCE 1 (bases 1 to 270)
 AUTHORS Herrmann, R. and Wong, J.F.
 TITLE Scorpion toxins
 JOURNAL Patent: US 6768002-A 32 27-JUL-2004;
 FEATURES source
 ORIGIN /organism="Hottentotta judaica"
 /mol_type="unassigned DNA"
 /db_xref="taxon:6863"

Query Match 22.8%; Score 40.8; DB 6; Length 270;
 Best Local Similarity 61.1%; Pred. No. 0.033; Mismatches 0; Indels 0; Gaps 0;
 Matches 66; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 70 ATTAATCCGGACTGCAATTAAAGATCTGTCAAAACAGGTGGATTACGGTATTGGTACG 129
 Db 131 ATCATGATTATGTCGGACATTAAACTACATGGAGTAATTGGGTATTTGGGG 190

Qy 130 CCTTCGAATCTGGTGATTCTGGTGAAGATGAAACGCTGAAGCT 177
 Db 191 TCACCTCGTGTGGTGAATATTGAAGAAGACATCAATT 238

RESULT 6
 LOCUS AR566416 DEFINITION Sequence 36 from patent US 6768002. DNA linear PAT 08-OCT-2004
 ACCESSION AR566416
 VERSION AR566416.1 GI:53983406
 KEYWORDS Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED
 REFERENCE 1 (bases 1 to 270)
 AUTHORS Herrmann, R. and Wong, J.F.
 TITLE Scorpion toxins
 JOURNAL Patent: US 6768002-A 36 27-JUL-2004;
 FEATURES source
 ORIGIN /organism="Hottentotta judaica"
 /mol_type="genomic DNA"
 /db_xref="taxon:6863"

Query Match 22.8%; Score 40.8; DB 6; Length 270;
 Best Local Similarity 61.1%; Pred. No. 0.033; Mismatches 0; Indels 0; Gaps 0;
 Matches 66; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 70 ATTAATCCGGACTGCAATTAAAGATCTGTCAAAACAGGTGGATTACGGTATTGGTACG 129
 Db 131 ATCATGATTATGTCGGACATTAAACTACATGGAGTAATTGGGTATTTGGGG 190

Qy 130 CCTTCGAATCTGGTGATTCTGGTGAAGATGAAACGCTGAAGCT 177
 Db 191 TCACCTCGTGTGGTGAATATTGAAGAAGACATCAATT 238

RESULT 9	AR566413	AR566413	Sequence 30 from patent US 6768002.	270 bp	DNA	linear	PAT 08-OCT-2004
DEFINITION							
ACCESSION	AR566413	GI:53983403					
VERSION	AR566413.1						
KEYWORDS	Scorpion toxins						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 270)						
AUTHORS	Herrmann,R. and Wong,J.F.						
TITLE	Scorpion Toxins						
JOURNAL	Patent : US 6768002-A 30 27-JUL-2004;						
FEATURES	Location/Qualifiers						
source	1..270 /organism="unknown" /mol_type="genomic DNA"						
ORIGIN							
Query Match	21.2%;	Score 38;	DB 6;	Length 270;			
Best Local Similarity	56.0%;	Pred. No.	0.28;				
Matches	93;	Conservative	0;	Mismatches	70;	Indels	3;
						Gaps	1;
Qy	12 CCGGGAACTTACCAACTTGATTCCTCCGACAAATACCTACTGCGCCCTTGGGAGAT	71					
Db	76 CCAGGAATTACCGATATCGRITATGGCTTGTACCTGATGTTTAATCAT	135					
Qy	72 AATCGGAACTGCAATTAAAGATCTGCAAGAACACGGTGTGATAACGGTACGCC	131					
Db	136 AAT..-TATTGTGGACATTTGTAAGTACATGGATAAAGTAGGTATGGTATGGTC	192					
Qy	132 TTCCGATGCTGCTGAATTCTGAAAGGTGAGAACGCTGAAGCT 177						
Db	193 ACCCTGTTGGTGTGAATATTGAAAGAACATGATGATATT	238					
RESULT 10	AX061768	AX061768	Sequence 30 from Patent WO0078957.	270 bp	DNA	linear	PAT 24-JAN-2001
DEFINITION							
ACCESSION	AX061768	GI:12539856					
VERSION	AX061768.1						
KEYWORDS							
ORGANISM	Hottentotta judaica						
REFERENCE	1. Herrmann,R., Lee,J.M. and Wong,J.F.						
AUTHORS	Scorpion Toxins from butiolus judaicus						
JOURNAL	Patent : WO 078957-A 30 28-DEC-2000;						
FEATURES	E.I. DU NEUMOUR AND COMPANY (US)						
source	1..270 /organism="Hottentotta judaica" /mol_type="unassigned DNA" /db_xref="taxon:8863"						
ORIGIN							
Query Match	21.2%;	Score 38;	DB 6;	Length 270;			
Best Local Similarity	56.0%;	Pred. No.	0.28;				
Matches	93;	Conservative	0;	Mismatches	70;	Indels	3;
						Gaps	1;
Qy	12 CCGGGAACTTACCAACTTGATTCCTCCGACAAATACCTACTGCGCCCTTGGGAGAT	71					
Db	76 CCAGGAATTACCGATATGGTACGTCTTATGATGCAACCTTTAATCAT	135					
Qy	72 AATCGGAACTGCAATTAAAGATCTGCAAGAACACGGTGTGATTACGGTACGCC	131					
Db	136 AAT..-TATTGTGGACATTTGTAAGTAGGTAAAGTAGGTGGTGGTC	192					
RESULT 11	AF491133	AF491133	Centruroides limpidus sodium-channel modifier toxin Cl17 precursor	316 bp	mRNA	linear	INV 12-FEB-2004
DEFINITION							
ACCESSION	AF491133	AF491133	Centruroides limpidus mRNA, complete cds.				
VERSION	AF491133.1	GI:31376361					
KEYWORDS							
SOURCE	Corona,M. and Possani,L.D.						
ORGANISM	Centruroides limpidus Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; Buthidae; Buthidae; Centruroides.						
REFERENCE	1 (bases 1 to 316)						
AUTHORS	Corona,M. and Possani,L.D.						
TITLE	Genes and peptides from the scorpion Centruroides limpidus						
JOURNAL	Unpublished						
FEATURES	Limpidus, that recognize Na(+)-channels						
source	2 (bases 1 to 316)						
REFERENCE	Corona,M. and Possani,L.D.						
AUTHORS	Direct Submission						
JOURNAL	Submitted (12-MAR-2002) Bioestructura Y Reconocimiento Molecular						
FEATURES	Instituto de Biologia, Av. Universidad 2001, Cuernavaca, Morelos 62210, Mexico						
source	Location/Qualifiers						
1..316	/organism="Centruroides limpidus limpidus"						
	/mol_type="mRNA"						
	/sub_species="limpidus"						
	/db_xref="taxon:29941"						
	5..262						
CDS	/note="preprotein"						
	/codon_start=1						
	/product="sodium-channel modifier toxin Cl17 precursor"						
	/protein_id="IAAP195081"						
	/db_xref="GI:31376362"						
	/translation="MNSLLMITPACLVLFGLTVWAKEGYLVNTYTGCKYICWKLGENDKCYC						
	IDBCKEKGAGYCYCFCYCEGFPEKNPKTPWLPNKTGGRK"						
	5..61						
	.259						
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ORIGIN							
Query Match	21.2%	Score 38;	DB 3;	Length 316;			
Best Local Similarity	60.8%	Pred. No. 0.27;					
Matches	62;	Conservative	0;	Mismatches	40;	Indels	0;
						Gaps	0;
Qy	48 TACCTGTGGCCCTTGGAGATAATCCGGACTGCAATTAGATGTCAGAAACACGGT	107					
Db	101 TACATTGTGGAAATGGAGAGAACAAATACTGATGATGTAAGAGATAGGA	160					
Qy	108 GTGGATTACGGTATTGGCTAGCCCTCCAATGGCTGGTGTGAA	149					
Db	161 GCTGGTACGGCTATTGGCTAGGTATTGGCTATGGAA	202					
RESULT 12							
DEFINITION							
ACCESSION	AY351304	AY351304	Centruroides sculpturatus isolate	192 bp	DNA	linear	INV 31-DEC-2003
VERSION							
KEYWORDS							
JOURNAL							
FEATURES							
source							
Qy	12 CCGGGAACTTACCAACTTGATTCCTCCGACAAATACCTACTGCGCCCTTGGGAGAT	71					
Db	76 CCAGGAATTACCGATATGGTACGTCTTATGATGCAACCTTTAATCAT	135					
Qy	72 AATCGGAACTGCAATTAAAGATCTGCAAGAACACGGTGTGATTACGGTACGCC	131					
Db	136 AAT..-TATTGTGGACATTTGTAAGTAGGTAAAGTAGGTGGTGGTC	192					

SOURCE Centruroides sculpturatus (bark scorpion)

ORGANISM Centruroides sculpturatus

Eukaryota; Metazoa; Arthropoda; Chelicera; Arachnida; Scorpiones;

Buthidae; Buthidae; Centruroides.

REFERENCE 1. (bases 1 to 192)

AUTHORS Zhu,S.

TITLE Alignment of beta-toxin nucleotide sequences

JOURNAL Unpublished

FEATURES source

REFERENCE 2. (bases 1 to 192)

AUTHORS Zhu,S.

TITLE Direct Submission

JOURNAL Submitted (24-JUL-2003) Leuven University, Lab of Toxicology, E van Evenstraat, Leuven, Flanders 3000, Belgium

Location/Qualifiers 1..192

/organism="Centruroides sculpturatus"

/mol type="genomic DNA"

/isolate="CsEv1b"

/db_xref="taxon:218467"

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/product="beta-toxin"

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/db_xref="GI:38017467"

/translation="KEGYLVKSDGCKYDCFWLGKNEHCDECKAKRNQGSYGYCYAFA CWCGLPBPSTPYPLPNSC"

ORIGIN

Query Match Score 36.8; DB 3; Length 192;

Best Local Similarity 73.4%; Pred. No. 0.69; Mismatches 0; Gaps 0;

Matches 47; Conservative 0; MisMatches 17; Indels 0; Gaps 0;

Qy 97 AGAAACACGGTGTGGATTACGGTTACGCCTTCATGCTGTTGAATTTCGTA 156

Db 92 AGAACCAAGGAGTAGTTACGGTTACGCCTTCATGCTGTTGAAGGTTGC 151

RESULT 13

AY351305

LOCUS AY351305 192 bp DNA linear INV 31-Dec-2003

DEFINITION Centruroides sculpturatus isolate CsEv1c beta-toxin gene, partial

cds

ACCESSION AV351305.1

VERSION GI:38017468

KEYWORDS

SOURCE

ORGANISM Centruroides sculpturatus (bark scorpion)

Eukaryota; Metazoa; Arthropoda; Chelicera; Arachnida; Scorpiones;

Buthidae; Buthidae; Centruroides.

REFERENCE 1. (bases 1 to 192)

AUTHORS Zhu,S.

TITLE Alignment of beta-toxin nucleotide sequences

JOURNAL Unpublished

FEATURES source

REFERENCE 2. (bases 1 to 192)

AUTHORS Zhu,S.

TITLE Direct Submission

JOURNAL Submitted (24-JUL-2003) Leuven University, Lab of Toxicology, E van Evenstraat, Leuven, Flanders 3000, Belgium

Location/Qualifiers 1..192

/organism="Centruroides sculpturatus"

/mol type="genomic DNA"

/isolate="CsEv1c"

/db_xref="taxon:218467"

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/product="beta-toxin"

<1..>192

ORIGIN

Query Match Score 36.8; DB 3; Length 192;

Best Local Similarity 73.4%; Pred. No. 0.69; Mismatches 0; Gaps 0;

Matches 47; Conservative 0; MisMatches 17; Indels 0; Gaps 0;

Qy 97 AGAAACACGGTGTGGATTACGGTTACGCCTTCATGCTGTTGAATTTCGTA 156

Db 92 AGAACCAAGGAGTAGTTACGGTTACGCCTTCATGCTGTTGAAGGTTGC 151

RESULT 15

mRNA

CDS

AY351307 LOCUS AY351307 192 bp DNA linear INV 31-DEC-2003
 DEFINITION Centroiooides sculpturatus isolate CsEvId beta-toxin gene, Partial
 Cds.

ACCESSION AY351307
 VERSION AY351307.1 GI:38017472

KEYWORDS Centroiooides sculpturatus (bark scorpion)

ORGANISM Centroiooides sculpturatus
 Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 Buthida; Buthoidea; Buthidae; Centroiooides.

REFERENCE 1. (bases 1 to 192)

AUTHORS Zhu S.

TITLE Alignment of beta-toxin nucleotide sequences
 Unpublished

JOURNAL REFERENCE 2. (bases 1 to 192)

AUTHORS Zhu,S.

TITLE Direct Submission (24-JUL-2003) Leuven University, Lab of Toxicology, E van
 JOURNAL Submitted (24-JUL-2003) Leuven University, Lab of Toxicology, E van
 Evenstraat, Leuven, Flanders 3000, Belgium

FEATURES Location/Qualifiers

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 /mol_type="Genomic DNA"
 /isolate="CsEvId"
 /db_xref="taxon:218467"
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mRNA

CDS

ORIGIN

Query Match Score 36.8; DB 3; Length 192;
 Best Local Similarity 73.4%; Pred. No. 0.69;
 Matches 47; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy	97 AGAACACCGTGTGGATTAGGGTATGGCTTCCAAATGTTGGAATTTCCTGA 156
Db	92 AGAACCAAGGGTAGTTAGGGTATGGCTTCCATGCTGGTGCAGGTTGC 151
Qy	157 AGGA 160
Db	152 CGGA 155

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